Human DNase I

```
LOCUS       HUMDNASEI    1039 bp    mRNA            PRI     06-MAR-1995
DEFINITION  Human DNase I mRNA, complete cds.
ACCESSION   M55983
VERSION     M55983.1  GI:181623
KEYWORDS    DNase I.
SOURCE      Human pancreus, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
  TITLE     Recombinant human DNase I reduces the viscosity of cystic fibrosis
            sputum
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE   91067672
FEATURES             Location/Qualifiers
     source          1..1039
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue_type="pancreas"
     sig peptide     160..225
                     /gene="DNase I"
     CDS             160..1008
                     /gene="DNase I"
                     /codon_start=1
                     /product="DNase I"
                     /protein_id="AAA63170.1"
                     /db_xref="GI:181624"
                     /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
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                     LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                     DAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
                     PDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYP
                     VEVMLK"
     gene            160..1008
                     /gene="DNase I"
     mat peptide     226..1005
                     /gene="DNase I"
                     /product="DNase I"
BASE COUNT      226 a    305 c    282 g    226 t
ORIGIN
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       61 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
      121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
      181 ggggcgctgc tggcactggc ggccctactg caggggccg tgtccctgaa gatcgcagcc
      241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
      301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
      361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
      421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
      481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
      541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc
      601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
      661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
      721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
      781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
      841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt
      901 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
      961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
     1021 cacaccagtt gaactgcag
//
```

Fig. 1

Human DNase I construct

```
LOCUS       MHDNASE.DN     783 bp    mRNA            PRI       06-MAR-1995
DEFINITION  Human DNase I mRNA, complete cds, Mature sequence modified to remove Nar1
site
ACCESSION   M55983
NID         g181623
KEYWORDS    DNase I.
SOURCE      Human pancreus, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
  TITLE     Recombinant human DNase I reduces the viscosity of cystic fibrosis
            sputum
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE   91067672
FEATURES             Location/Qualifiers
     source          1. .1039
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue_type="pancreas"
     sig_peptide     160. .225
                     /gene="DNase I"
     CDS             160. .1008
                     /gene="DNase I"
                     /codon_start=1
                     /product="DNase I"
                     /db_xref="PID:g181624"
                     /translation="LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSH
                     LTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYYDDGCE
                     PCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGL
                     EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
                     MLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK"
     gene            160. .1008
                     /gene="DNase I"
     mat_peptide     226. .1005
                     /gene="DNase I"
                     /product="DNase I"
BASE COUNT      168 a    236 c    220 g    159 t
ORIGIN
        1 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
       61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      121 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
      241 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
      301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
      361 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
      421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
      481 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
      541 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
      601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
      661 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
      721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
      781 TGA
//
```

Fig. 2(A)

```
LOCUS       PAS155_GB.     858 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
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                     /note="160 to 225 of Untitled1"
     frag            <10..>75
                     /note="1 to 1039 of M55983.DNA [Split]"
     source          <10..>75
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue_type="pancreas [Split]"
     sig_peptide     10..75
                     /gene="DNase I"
     CDS             10..>75
                     /gene="DNase I"
                     /codon_start="1"
                     /product="DNase I"
                     /db_xref="PID:g181624"
/translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
SYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY
LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
D... [Split]"
     gene            10..>75
                     /gene="DNase I [Split]"
     frag            76..858
                     /note="1 to 783 of mod humanDNAseI"
     frag            76..858
                     /note="1 to 72 of 104linker"
     frag            join(76..>129,<131..147)
                     /note="1 to 72 of 103linker [Split]"
     frag            join(76..>126,<127..>129,<131..147)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      177 A    260 C    251 G    170 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG
       61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
      121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
      181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
      241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
      301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
      361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
      421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
      481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
      541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
      601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
      661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
      721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
      781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
      841 GAGGTGATGC TGAAGTGA
//
```

Fig. 2(B)

pAS6 – light chain

```
LOCUS       HMFG1LC2.D    721 bp    DNA                    18-AUG-1998
DEFINITION  HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
ACCESSION
KEYWORDS
SOURCE
  ORGANISM
REFERENCE   1  (BASES 1 TO 342)
  AUTHORS   VERHOEYEN ET AL
  TITLE     CONSTRUCTION OF RESHAPED HMFG1 ETC
  JOURNAL   IMMUNOL. (1993):78, 364-370
COMMENT     SCANNED IN FROM JOURNAL
FEATURES
  SITES

This is the sequence of the HMFG1 light chain gene with the
Vnp  leader sequence attached. Translate from
residue 1. Note residue 399 is T > A in all clones leading
to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT      197 a    202 c    182 g    140 t
ORIGIN           ?
```

x LEADER SEQ

```
      1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCGAC
     61 ATCCAGATGA CCCAGAGCCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
    121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG
    181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
    241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC
    301 AGCAGCCTCC AGCCAGAGGA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
    361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
    421 TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG
    481 CTGAATAACT TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA
    541 TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
    601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA CGCCTGCGAA
    661 GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT TCAACAGGGG AGAGTGTTAG
        721 A
//
```

Fig. 3(A)

```
LOCUS        HHMFG1KLC_     730 BP SS-DNA              SYN       29-AUG-2000
DEFINITION   -
ACCESSION    -
KEYWORDS     -
SOURCE       -
FEATURES             Location/Qualifiers
     frag            10..730
                     /note="1 to 721 of hHMFG1light chain"
     frag            10..730
                     /note="1 to 72 of 104linker"
     frag            join(10..>63,<65..81)
                     /note="1 to 72 of 103linker [Split]"
     frag            join(10..>60,<61..>63,<65..81)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      198 A    208 C    184 G    140 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
      121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
      181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
      241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
      301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
      361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
      421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
      481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
      541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
      601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
      661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
      721 GAGTGTTAGA
//
```

Fig. 3(B)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCIILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL
LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT
DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC

Fig. 3(C)

pAS6 – heavy chain

LOCUS HHMFG1HC.D 1404 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain
ACCESSION HHMFG1H
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT VH domain SCANNED IN FROM JOURNAL
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 333 a 439 c 379 g 253 t
ORIGIN ?

LEADER

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA
```

Antibody DNase Fusions Made Here
(eg pAS34----39.)

End of lower hinge region of heavy chain. PAPE Amino Acid Seq. Fab'$_2$ fusions were made at this point.

Those with HYBRID HINGES are altered further up i.e.

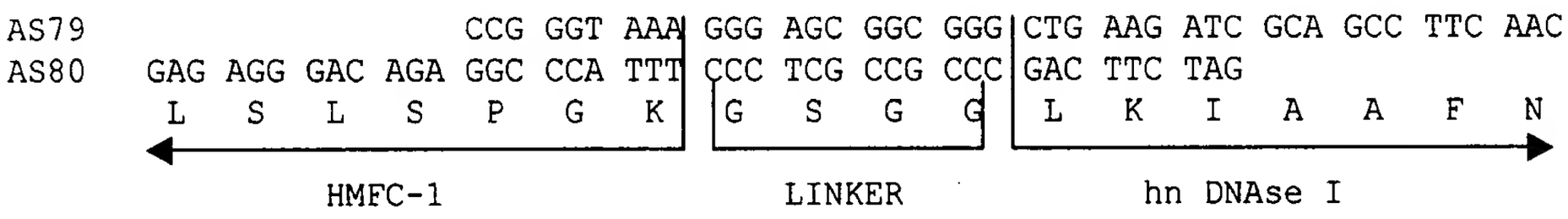
This part GACAAAACTGACACA
D K T H T

After this sequence you get the HYBRID HINGE + LINKER SEQUENCES
Then DNAse I (eg Fab-DNase construct pAS302)

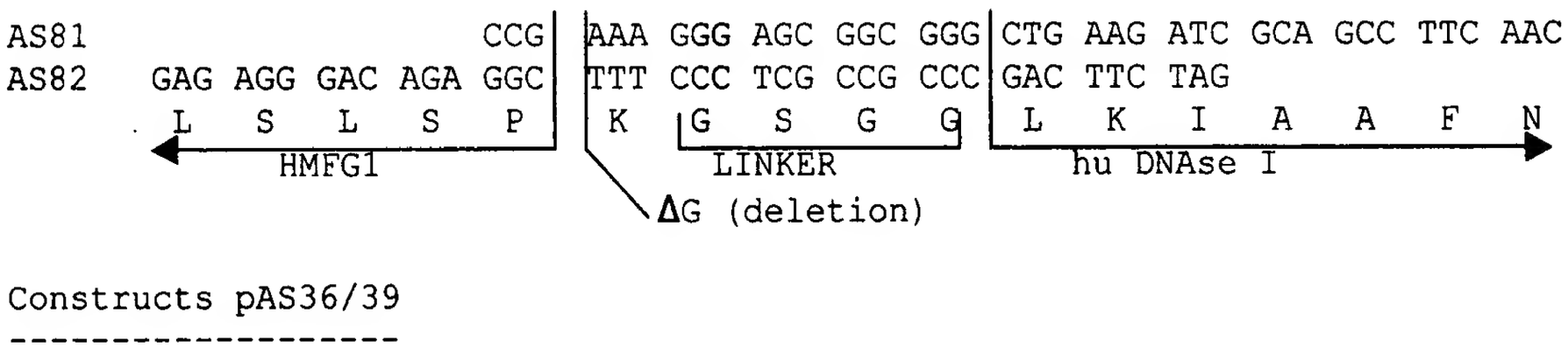
Fig. 3(D)

Oligos involved in the fusion of whole antibody-DNase

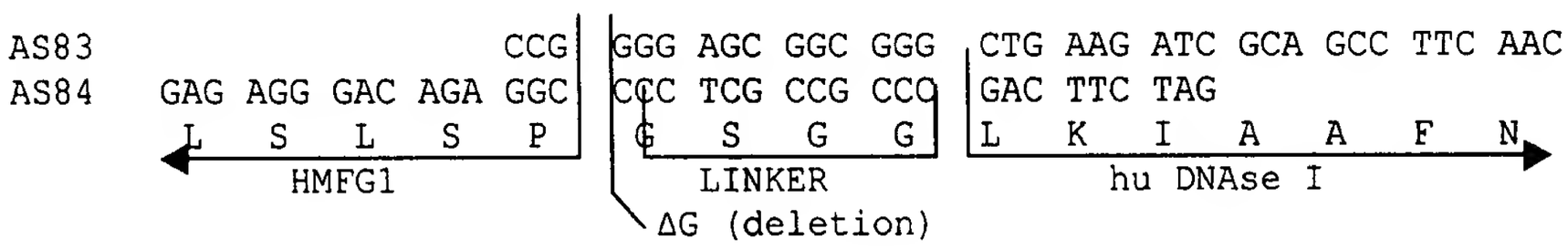
Constructs pAS34/37



Constructs pAS35/38



Constructs pAS36/39



Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

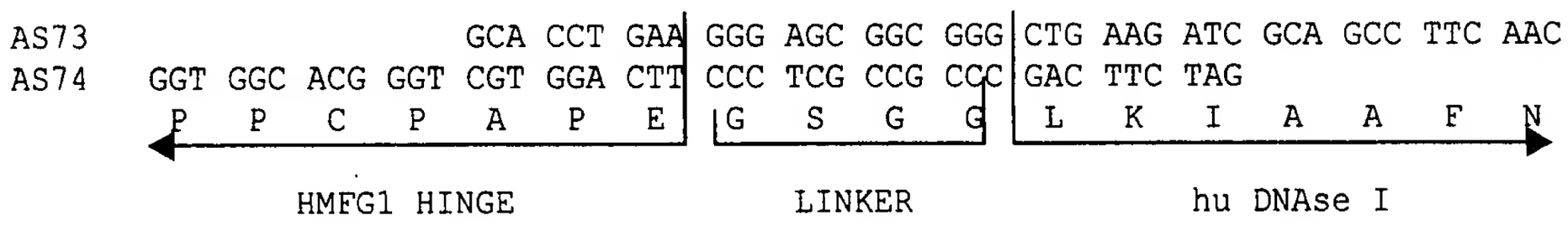
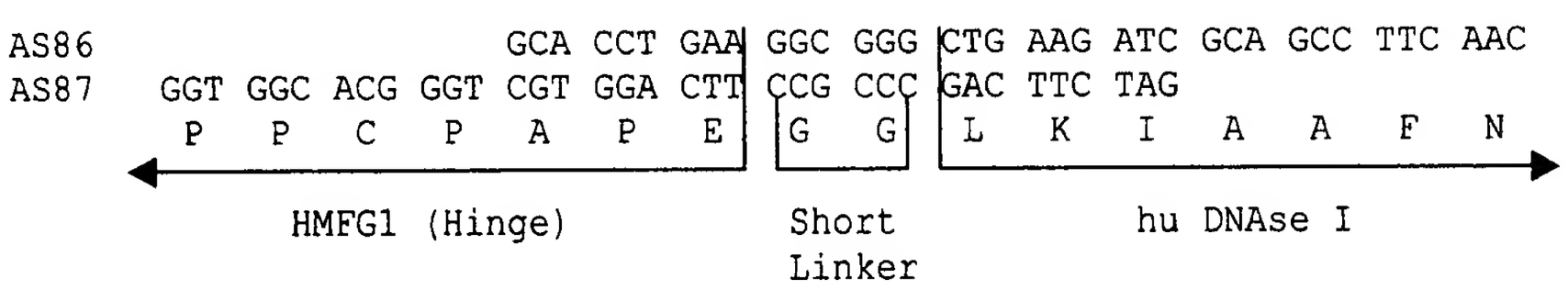


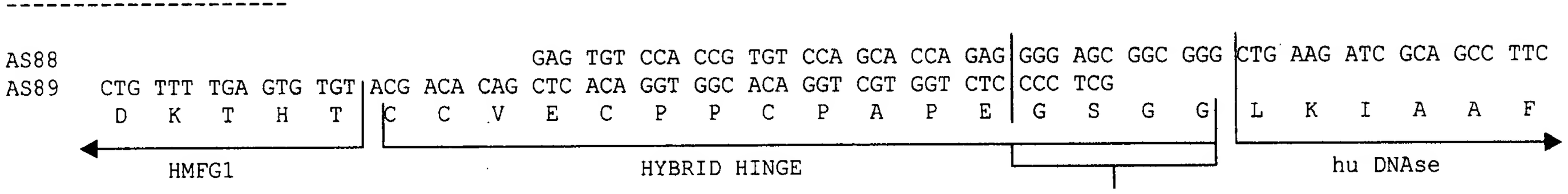
Fig. 4(A)

Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs pAS101/105



Constructs pAS102/106



Constructs pAS103/107

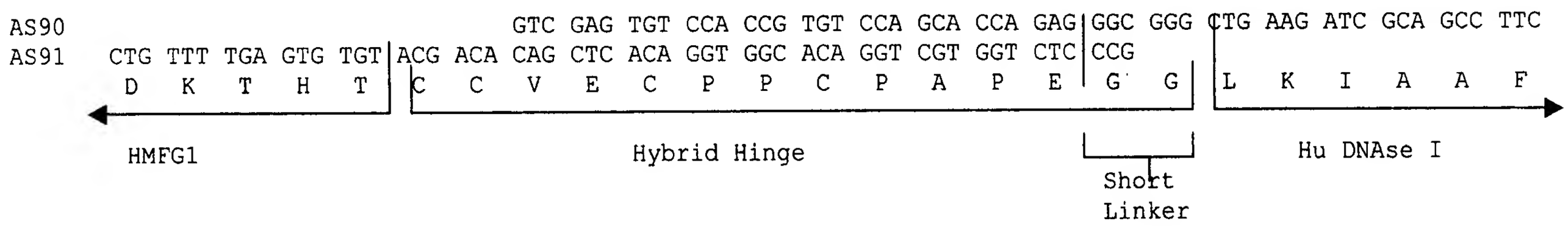


Fig. 4(B)

pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 434 g 308 t
ORIGIN

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   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA
//
```

Fig. 5(A)

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LOCUS       FDDNASE23_    1554 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
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     frag            721..786
                     /note="1 to 66 of 23/27linker"
     frag            join(721..>735,<736..786)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      344 A    466 C    435 G    309 T      0 OTHER
ORIGIN      -
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC
      781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
      841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
      901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
      961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
     1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
     1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
     1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
     1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
     1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
     1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
     1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
     1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
     1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA
//
```

Fig. 5(B)

```
LOCUS       FDDNASE23K   1563 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1563
                     /note="1 to 1554 of FdDNase23correct"
     frag            join(10..>729,<796..1563)
                     /note="1 to 1554 of 23.dna [Split]"
     frag            730..795
                     /note="1 to 66 of 23/27linker"
     frag            join(730..>744,<745..795)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      345 A    472 C    437 G    309 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
     1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
     1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
     1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
     1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
     1561 TGA
//
```

Fig. 5(C)

```
                9           18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99          108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 5(D)

(Sheet 1 of 3)

```
          603             612             621             630             639             648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657             666             675             684             693             702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711             720             729             738             747             756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765             774             783             792             801             810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   S   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E

          819             828             837             846             855             864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R

          873             882             891             900             909             918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   D   I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G

          927             936             945             954             963             972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   L   L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V

          981             990             999            1008            1017            1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   E   P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R

         1035            1044            1053            1062            1071            1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P

         1089            1098            1107            1116            1125            1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   G   N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R

         1143            1152            1161            1170            1179            1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   T   E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D

         1197            1206            1215            1224            1233            1242
```

Fig. 5(D)

(Sheet 2 of 3)

```
GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K

        1251        1260        1269        1278        1287        1296
TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y

        1305        1314        1323        1332        1341        1350
GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q

        1359        1368        1377        1386        1395        1404
TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y

        1413        1422        1431        1440        1449        1458
GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S

        1467        1476        1485        1494        1503        1512
GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q

        1521        1530        1539        1548
GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   I   S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 5(D)

(Sheet 3 of 3)

pAS27

LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 446 g 310 t
ORIGIN

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   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
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 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
1561 CCCAAAAAGA AGCGCAAGGT TTGA
```

//

Fig. 6(A)

```
LOCUS       FDDNASE27_   1584 BP SS-DNA           SYN      25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<787..1584)
                     /note="1 to 1584 of 27.dna [Split]"
     frag            721..786
                     /note="1 to 66 of 23/27linker"
     frag            join(721..>735,<736..786)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT     354 A    472 C    447 G    311 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
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      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC
      781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
      841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
      901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
      961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
     1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
     1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
     1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
     1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
     1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
     1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
     1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
     1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
     1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
     1561 CCCAAAAAGA AGCGCAAGGT TTGA
//
```

Fig. 6(B)

```
LOCUS       FDDNASE27K   1593 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1593
                     /note="1 to 1584 of FdDNase27correct"
     frag            join(10..>729,<796..1593)
                     /note="1 to 1584 of 27.dna [Split]"
     frag            730..795
                     /note="1 to 66 of 23/27linker"
     frag            join(730..>744,<745..795)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      355 A    478 C    449 G    311 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
     1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
     1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
     1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
     1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
     1561 GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT TGA
//
```

Fig. 6(C)

```
                9           18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99         108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 6(D)

(Sheet 1 of 3)

```
          603           612           621           630           639           648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657           666           675           684           693           702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711           720           729           738           747           756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765           774           783           792           801           810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   S   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E

          819           828           837           846           855           864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R

          873           882           891           900           909           918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   D   I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G

          927           936           945           954           963           972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   L   L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V

          981           990           999          1008          1017          1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   E   P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R

         1035          1044          1053          1062          1071          1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P

         1089          1098          1107          1116          1125          1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   G   N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R

         1143          1152          1161          1170          1179          1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   T   E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D

         1197          1206          1215          1224          1233          1242
```

Fig. 6(D)

(Sheet 2 of 3)

```
GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K

       1251        1260        1269        1278        1287        1296
TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y

       1305        1314        1323        1332        1341        1350
GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q

       1359        1368        1377        1386        1395        1404
TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y

       1413        1422        1431        1440        1449        1458
GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S

       1467        1476        1485        1494        1503        1512
GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q

       1521        1530        1539        1548        1557        1566
GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   I   S   D   H   Y   P   V   E   V   M   L   K   G   G   G   P   K

       1575        1584
AAG AAG CGC AAG GTT TGA 3'
--- --- --- --- --- ---
 K   K   R   K   V   *
```

Fig. 6D

(Sheet 3 of 3)

pAS34

```
LOCUS       PAS34.DNA    2196 bp        2196 bp  2196 bp  DNA   14-AUG-1998
DEFINITION  HUMANISED HMFG1 heavy chain fused to human DNAse construct 34
DEFINITION  Clone 16.4.2 (same as hcdnase1.dna template file)
REFERENCE
  AUTHORS   VERHOEYEN ET AL
  TITLE     CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL   IMMUNOL. (1993):78, 364-370
COMMENT     Human DNAse sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT     The fusion was made using overlapping oligos AS79 and AS80
FEATURES    AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES    Residue 963 is G > T leading to silent mutation in all clones
  SITES     Note
BASE COUNT      501 a    677 c    607 g    411 t
ORIGIN          ?

        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
      781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
      841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
      901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
      961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
     1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
     1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
     1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
     1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
     1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
     1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
     1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
     1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
     1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
     1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
     1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
     1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
     1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
     1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
     1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
     1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
     1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
     2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
     2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
     2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA
//
```

Fig. 7(A)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

              603                 612                 621                 630                 639                 648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

              657                 666                 675                 684                 693                 702
```

Fig. 7(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711             720             729             738             747             756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765             774             783             792             801             810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

          819             828             837             846             855             864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

          873             882             891             900             909             918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

          927             936             945             954             963             972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

          981             990             999            1008            1017            1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

         1035            1044            1053            1062            1071            1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

         1089            1098            1107            1116            1125            1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

         1143            1152            1161            1170            1179            1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

         1197            1206            1215            1224            1233            1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

         1251            1260            1269            1278            1287            1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

         1305            1314            1323            1332            1341            1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 7(B)

(Sheet 2 of 4)

```
      1359       1368       1377       1386       1395       1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   G   K   G

      1413       1422       1431       1440       1449       1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K

      1467       1476       1485       1494       1503       1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D

      1521       1530       1539       1548       1557       1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L

      1575       1584       1593       1602       1611       1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E

      1629       1638       1647       1656       1665       1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D

      1683       1692       1701       1710       1719       1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G

      1737       1746       1755       1764       1773       1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T

      1791       1800       1809       1818       1827       1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V

      1845       1854       1863       1872       1881       1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G

      1899       1908       1917       1926       1935       1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R

      1953       1962       1971       1980       1989       1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L

      2007       2016       2025       2034       2043       2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R
```

Fig. 7(B)

(Sheet 3 of 4)

```
          2061                2070                2079                2088                2097                2106
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L

          2115                2124                2133                2142                2151                2160
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I

          2169                2178                2187                2196
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- ---
 S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 7(B)

(Sheet 4 of 4)

pAS35

```
LOCUS       PAS35.DNA    2193 bp   2193 bp    DNA              14-AUG-1998
DEFINITION  HUMANISED HMFG1 heavy chain fused to human DNAse construct 35
DEFINITION  Clone 17.12.1 with silent K to K mutation (1398 A > G)
REFERENCE
  AUTHORS   VERHOEYEN ET AL
  TITLE     CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL   IMMUNOL. (1993):78, 364-370
COMMENT     Human DNAse sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT     The fusion was made using overlapping oligos AS81 and AS82
FEATURES    AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES    Residue 963 is G > T leading to silent mutation in all clones
FEATURES    In 17.12.1 residue 1398 is A > G (silent K to K mutation)
  SITES     Note
BASE COUNT      500 a    677 c    606 g    410 t
ORIGIN          ?

       1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
      61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
     121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
     181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
     241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
     301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
     361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
     421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
     481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
     541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
     601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
     661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
     721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
     781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
     841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
     901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
     961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
    1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
    1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
    1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
    1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
    1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
    1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
    1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
    1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
    1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
    1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
    1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT
    1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
    1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT
    1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
    1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
    1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
    1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
    2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
    2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
    2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA
//
```

Fig. 8(A)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

                63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

               117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

               171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

               225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

               279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

               333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

               387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

               441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

               495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

               549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

               603                 612                 621                 630                 639                 648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

               657                 666                 675                 684                 693                 702
```

Fig. 8(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

        711         720         729         738         747         756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

        765         774         783         792         801         810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

        819         828         837         846         855         864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

        873         882         891         900         909         918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

        927         936         945         954         963         972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

        981         990         999        1008        1017        1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

       1035        1044        1053        1062        1071        1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

       1089        1098        1107        1116        1125        1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

       1143        1152        1161        1170        1179        1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

       1197        1206        1215        1224        1233        1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

       1251        1260        1269        1278        1287        1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

       1305        1314        1323        1332        1341        1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 8(B)

(Sheet 2 of 4)

```
      1359        1368        1377        1386        1395        1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   K   G   S

      1413        1422        1431        1440        1449        1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K   M

      1467        1476        1485        1494        1503        1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D   I

      1521        1530        1539        1548        1557        1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L   L

      1575        1584        1593        1602        1611        1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E   P

      1629        1638        1647        1656        1665        1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D   Q

      1683        1692        1701        1710        1719        1728
GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G   N

      1737        1746        1755        1764        1773        1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T   E

      1791        1800        1809        1818        1827        1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V   A

      1845        1854        1863        1872        1881        1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G   L

      1899        1908        1917        1926        1935        1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R   P

      1953        1962        1971        1980        1989        1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L   I

      2007        2016        2025        2034        2043        2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R   I
```

Fig. 8(B)

(Sheet 3 of 4)

```
          2061                2070                2079                2088                2097                2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L   P

          2115                2124                2133                2142                2151                2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I   S

          2169                2178                2187
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- ---
 D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 8(B)

(Sheet 4 of 4)

pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse - construct 36
DEFINITION Clone 18.24.1 with residue 1392 T > C
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 498 a 678 c 605 g 409 t
ORIGIN ?

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

Fig. 9(A)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

                63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

                117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

                171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

                225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

                279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

                333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

                387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

                441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

                495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

                549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

                603                 612                 621                 630                 639                 648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

                657                 666                 675                 684                 693                 702
```

Fig. 9(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711         720         729         738         747         756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765         774         783         792         801         810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

          819         828         837         846         855         864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

          873         882         891         900         909         918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

          927         936         945         954         963         972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

          981         990         999        1008        1017        1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

         1035        1044        1053        1062        1071        1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

         1089        1098        1107        1116        1125        1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

         1143        1152        1161        1170        1179        1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

         1197        1206        1215        1224        1233        1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

         1251        1260        1269        1278        1287        1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

         1305        1314        1323        1332        1341        1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 9(B)

(Sheet 2 of 4)

```
        1359        1368        1377        1386        1395        1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   G   S   G

        1413        1422        1431        1440        1449        1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K   M   S

        1467        1476        1485        1494        1503        1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D   I   A

        1521        1530        1539        1548        1557        1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L   L   D

        1575        1584        1593        1602        1611        1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E   P   L

        1629        1638        1647        1656        1665        1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D   Q   V

        1683        1692        1701        1710        1719        1728
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G   N   D

        1737        1746        1755        1764        1773        1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T   E   V

        1791        1800        1809        1818        1827        1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V   A   E

        1845        1854        1863        1872        1881        1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G   L   E

        1899        1908        1917        1926        1935        1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R   P   S

        1953        1962        1971        1980        1989        1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L   I   P

        2007        2016        2025        2034        2043        2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R   I   V
```

Fig. 9(B)

(Sheet 3 of 4)

```
        2061          2070          2079          2088          2097          2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L   P   F

        2115          2124          2133          2142          2151          2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I   S   D

        2169          2178          2187
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- ---
 H   Y   P   V   E   V   M   L   K   *
```

Fig. 9(B)
(Sheet 4 of 4)

pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 37
DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) plus NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS79 and AS80
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 511 a 683 c 619 g 413 t
ORIGIN ?

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAAA GAAGCGCAAG
2221 GTTTGA
```

NLS

//

Fig. 10(A)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

                63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

                117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

                171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

                225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

                279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

                333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

                387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

                441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

                495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

                549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

                603                 612                 621                 630                 639                 648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

                657                 666                 675                 684                 693                 702
```

Fig. 10(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

        711         720         729         738         747         756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

        765         774         783         792         801         810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

        819         828         837         846         855         864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

        873         882         891         900         909         918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

        927         936         945         954         963         972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

        981         990         999        1008        1017        1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

       1035        1044        1053        1062        1071        1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

       1089        1098        1107        1116        1125        1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

       1143        1152        1161        1170        1179        1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

       1197        1206        1215        1224        1233        1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

       1251        1260        1269        1278        1287        1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

       1305        1314        1323        1332        1341        1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 10(B)

(Sheet 2 of 4)

```
      1359        1368        1377        1386        1395        1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   G   K   G

      1413        1422        1431        1440        1449        1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K

      1467        1476        1485        1494        1503        1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D

      1521        1530        1539        1548        1557        1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L

      1575        1584        1593        1602        1611        1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E

      1629        1638        1647        1656        1665        1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D

      1683        1692        1701        1710        1719        1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G

      1737        1746        1755        1764        1773        1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T

      1791        1800        1809        1818        1827        1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V

      1845        1854        1863        1872        1881        1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G

      1899        1908        1917        1926        1935        1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R

      1953        1962        1971        1980        1989        1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L

      2007        2016        2025        2034        2043        2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R
```

Fig. 10(B)

(Sheet 3 of 4)

```
        2061            2070            2079            2088            2097            2106
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L

        2115            2124            2133            2142            2151            2160
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I

        2169            2178            2187            2196            2205            2214
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   D   H   Y   P   V   E   V   M   L   K   G   G   G   P   K   K   K

        2223
CGC AAG GTT TGA 3'
--- --- --- ---
 R   K   V   *
```

Fig. 10(B)

(Sheet 4 of 4)

pAS38

```
LOCUS       PAS38.DNA    2223 bp   2193 bp    DNA              14-AUG-1998
DEFINITION  HUMANISED HMFG1 heavy chain fused to human DNAse construct 38
DEFINITION  Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
REFERENCE
  AUTHORS   VERHOEYEN ET AL
  TITLE     CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL   IMMUNOL. (1993):78, 364-370
COMMENT     Human DNAse sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT     The fusion was made using overlapping oligos AS81 and AS82
FEATURES    AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES    Residue 963 is G > T leading to silent mutation in all clones
FEATURES    In 17.12.1 residue 1398 is A > G (silent K to K mutation)
  SITES     Note
BASE COUNT      510 a    683 c    618 g    412 t
ORIGIN          ?

        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
      781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
      841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
      901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
      961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
     1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
     1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
     1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
     1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
     1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
     1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
     1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
     1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
     1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
     1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
     1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT
     1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
     1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT
     1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
     1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
     1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
     1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
     2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
     2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
     2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT
     2221 TGA
//
```

NLS

Fig. 11(A)

```
                9          18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99         108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

              603         612         621         630         639         648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

              657         666         675         684         693         702
```

Fig. 11(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

        711         720         729         738         747         756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

        765         774         783         792         801         810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

        819         828         837         846         855         864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

        873         882         891         900         909         918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

        927         936         945         954         963         972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

        981         990         999        1008        1017        1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

       1035        1044        1053        1062        1071        1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

       1089        1098        1107        1116        1125        1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

       1143        1152        1161        1170        1179        1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

       1197        1206        1215        1224        1233        1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

       1251        1260        1269        1278        1287        1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

       1305        1314        1323        1332        1341        1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 11(B)

(Sheet 2 of 4)

```
      1359        1368        1377        1386        1395        1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   K   G   S

      1413        1422        1431        1440        1449        1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K   M

      1467        1476        1485        1494        1503        1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D   I

      1521        1530        1539        1548        1557        1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L   L

      1575        1584        1593        1602        1611        1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E   P

      1629        1638        1647        1656        1665        1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D   Q

      1683        1692        1701        1710        1719        1728
GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G   N

      1737        1746        1755        1764        1773        1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T   E

      1791        1800        1809        1818        1827        1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V   A

      1845        1854        1863        1872        1881        1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G   L

      1899        1908        1917        1926        1935        1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R   P

      1953        1962        1971        1980        1989        1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L   I

      2007        2016        2025        2034        2043        2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R   I
```

Fig. 11(C)

(Sheet 3 of 4)

```
          2061           2070           2079           2088           2097           2106
GTG  GTT  GCA  GGG  ATG  CTG  CTC  CGA  GGG  GCC  GTT  GTT  CCC  GAC  TCG  GCT  CTT  CCC
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 V    V    A    G    M    L    L    R    G    A    V    V    P    D    S    A    L    P

          2115           2124           2133           2142           2151           2160
TTT  AAC  TTC  CAG  GCT  GCC  TAT  GGC  CTG  AGT  GAC  CAA  CTG  GCC  CAA  GCC  ATC  AGT
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 F    N    F    Q    A    A    Y    G    L    S    D    Q    L    A    Q    A    I    S

          2169           2178           2187           2196           2205           2214
GAC  CAC  TAT  CCA  GTG  GAG  GTG  ATG  CTG  AAG  GGG  GGC  GGA  CCC  AAA  AAG  AAG  CGC
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 D    H    Y    P    V    E    V    M    L    K    G    G    G    P    K    K    K    R

          2223
AAG  GTT  TGA 3'
---  ---  ---
 K    V    *
```

Fig. 11(D)

(Sheet 4 of 4)

pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse - construct 39
DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 508 a 684 c 617 g 411 t
ORIGIN ?

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA
//
```

Fig. 12(A)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

                63                  72                  81                  90                  99                  108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

                117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

                171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

                225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

                279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

                333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

                387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

                441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

                495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

                549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G

                603                 612                 621                 630                 639                 648
    CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

                657                 666                 675                 684                 693                 702
```

Fig. 12(B)

(Sheet 1 of 4)

```
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

        711         720         729         738         747         756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

        765         774         783         792         801         810
GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T

        819         828         837         846         855         864
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H

        873         882         891         900         909         918
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N

        927         936         945         954         963         972
GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S

        981         990         999        1008        1017        1026
GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K

       1035        1044        1053        1062        1071        1080
GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K

       1089        1098        1107        1116        1125        1134
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L

       1143        1152        1161        1170        1179        1188
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D

       1197        1206        1215        1224        1233        1242
ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T

       1251        1260        1269        1278        1287        1296
CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V

       1305        1314        1323        1332        1341        1350
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E
```

Fig. 12(B)

(Sheet 2 of 4)

```
      1359        1368        1377        1386        1395        1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P   G   S   G

      1413        1422        1431        1440        1449        1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K   M   S

      1467        1476        1485        1494        1503        1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D   I   A

      1521        1530        1539        1548        1557        1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L   L   D

      1575        1584        1593        1602        1611        1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E   P   L

      1629        1638        1647        1656        1665        1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D   Q   V

      1683        1692        1701        1710        1719        1728
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G   N   D

      1737        1746        1755        1764        1773        1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T   E   V

      1791        1800        1809        1818        1827        1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V   A   E

      1845        1854        1863        1872        1881        1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G   L   E

      1899        1908        1917        1926        1935        1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R   P   S

      1953        1962        1971        1980        1989        1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L   I   P

      2007        2016        2025        2034        2043        2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R   I   V
```

Fig. 12(B)

(Sheet 3 of 4)

```
          2061          2070          2079          2088          2097          2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L   P   F

          2115          2124          2133          2142          2151          2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I   S   D

          2169          2178          2187          2196          2205          2214
CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   Y   P   V   E   V   M   L   K   G   G   G   P   K   K   K   R   K

GTT TGA 3'
--- ---
 V   *
```

Fig. 12(B)
(Sheet 4 of 4)

pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 343 a 467 c 430 g 308 t
ORIGIN

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   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
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//

Fig. 13(A)

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LOCUS       FDDNASE101    1548 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<781..1548)
                     /note="1 to 1548 of PAS101.dna [Split]"
     frag            721..780
                     /note="1 to 60 of 101/105linker"
     frag            join(721..>735,<736..>759,<760..>780)
                     /note="1 to 80 of 102linker [Split]"
BASE COUNT      343 A    465 C    431 G    309 T      0 OTHER
ORIGIN      -
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
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     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
     1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
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Fig. 13(B)

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LOCUS       FDDNASE101    1557 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
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                     /note="1 to 1548 of FdDNase101correct"
     frag            join(10..>729,<790..1557)
                     /note="1 to 1548 of PAS101.dna [Split]"
     frag            730..789
                     /note="1 to 60 of 101/105linker"
     frag            join(730..>744,<745..>768,<769..>789)
                     /note="1 to 80 of 102linker [Split]"
BASE COUNT      344 A    471 C    433 G    309 T      0 OTHER
ORIGIN      -
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
     1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
     1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
     1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
     1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA
//
```

Fig. 13(C)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 13(D)

(Sheet 1 of 3)

```
          603                 612                 621                 630                 639                 648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657                 666                 675                 684                 693                 702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711                 720                 729                 738                 747                 756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765                 774                 783                 792                 801                 810
GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K

          819                 828                 837                 846                 855                 864
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D

          873                 882                 891                 900                 909                 918
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L

          927                 936                 945                 954                 963                 972
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E

          981                 990                 999                1008                1017                1026
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D

         1035                1044                1053                1062                1071                1080
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G

         1089                1098                1107                1116                1125                1134
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T

         1143                1152                1161                1170                1179                1188
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V

         1197                1206                1215                1224                1233                1242
```

Fig. 13(D)

(Sheet 2 of 3)

```
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G

       1251        1260        1269        1278        1287        1296
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R

       1305        1314        1323        1332        1341        1350
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L

       1359        1368        1377        1386        1395        1404
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R

       1413        1422        1431        1440        1449        1458
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L

       1467        1476        1485        1494        1503        1512
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I

       1521        1530        1539        1548
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- ---
 S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 13(D)
(Sheet 3 of 3)

pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna) (See Figure 2)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 345 a 469 c 440 g 312 t
ORIGIN

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 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
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1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
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1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA
//
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Fig. 14(A)

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LOCUS       FDDNASE102    1566 BP SS-DNA              SYN        23-MAR-2001
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
BASE COUNT       345 A     468 C     440 G     313 T        0 OTHER
ORIGIN      -
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      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGTGA
//
```

Fig. 14(B)

pAS302

```
LOCUS       FDDNASE302    1575 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1575
                     /note="1 to 1566 of FdDNase102correct"
BASE COUNT      346 A    474 C    442 G    313 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
     1561 GTGATGCTGA AGTGA
//
```

Fig. 14(C)

```
                9           18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99         108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 14(D)

(Sheet 1 of 3)

```
          603             612             621             630             639             648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657             666             675             684             693             702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711             720             729             738             747             756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   C   V   E   C   P   P

          765             774             783             792             801             810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   A   P   E   G   S   G   G   L   K   I   A   A   F   N   I   Q

          819             828             837             846             855             864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   F   G   E   T   K   M   S   N   A   T   L   V   S   Y   I   V   Q

          873             882             891             900             909             918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   L   S   R   Y   D   I   A   L   V   Q   E   V   R   D   S   H   L

          927             936             945             954             963             972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   A   V   G   K   L   L   D   N   L   N   Q   D   A   P   D   T   Y

          981             990             999            1008            1017            1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   Y   V   V   S   E   P   L   G   R   N   S   Y   K   E   R   Y   L

         1035            1044            1053            1062            1071            1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   V   Y   R   P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D

         1089            1098            1107            1116            1125            1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   C   E   P   C   G   N   D   T   F   N   R   E   P   A   I   V   R

         1143            1152            1161            1170            1179            1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   F   S   R   F   T   E   V   R   E   F   A   I   V   P   L   H   A

         1197            1206            1215            1224            1233            1242
```

Fig. 14(D)

(Sheet 2 of 3)

```
GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   P   G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D

       1251        1260        1269        1278        1287        1296
GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   Q   E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A

       1305        1314        1323        1332        1341        1350
GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   C   S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S

       1359        1368        1377        1386        1395        1404
CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   T   F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T

       1413        1422        1431        1440        1449        1458
CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   C   A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V

       1467        1476        1485        1494        1503        1512
GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   P   D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D

       1521        1530        1539        1548        1557        1566
CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   L   A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 14(D)
(Sheet 3 of 3)

pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 436 g 312 t
ORIGIN

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
//
```

Fig. 15(A)

```
LOCUS       FDDNASE103    1560 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<793..1560)
                     /note="1 to 1560 of PAS103.dna [Split]"
     frag            721..792
                     /note="1 to 72 of 103/107linker"
     frag            join(721..>771,<772..792)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      344 A    467 C    436 G    313 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
//
```

Fig. 15(B)

```
LOCUS       FDDNASE103   1569 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1569
                     /note="1 to 1560 of FdDNase103correct"
     frag            join(10..>729,<802..1569)
                     /note="1 to 1560 of PAS103.dna [Split]"
     frag            730..801
                     /note="1 to 72 of 103/107linker"
     frag            join(730..>780,<781..801)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      345 A    473 C    438 G    313 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
     1561 CTGAAGTGA
//
```

Fig. 15(C)

```
                9           18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99          108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 15(D)

(Sheet 1 of 3)

```
          603                 612                 621                 630                 639                 648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657                 666                 675                 684                 693                 702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711                 720                 729                 738                 747                 756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   C   V   E   C   P   P

          765                 774                 783                 792                 801                 810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   A   P   E   G   G   L   K   I   A   A   F   N   I   Q   T   F

          819                 828                 837                 846                 855                 864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   E   T   K   M   S   N   A   T   L   V   S   Y   I   V   Q   I   L

          873                 882                 891                 900                 909                 918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   Y   D   I   A   L   V   Q   E   V   R   D   S   H   L   T   A

          927                 936                 945                 954                 963                 972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   G   K   L   L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y

          981                 990                 999                1008                1017                1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   V   S   E   P   L   G   R   N   S   Y   K   E   R   Y   L   F   V

         1035                1044                1053                1062                1071                1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   R   P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C

         1089                1098                1107                1116                1125                1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   P   C   G   N   D   T   F   N   R   E   P   A   I   V   R   F   F

         1143                1152                1161                1170                1179                1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   F   T   E   V   R   E   F   A   I   V   P   L   H   A   A   P

         1197                1206                1215                1224                1233                1242
```

Fig. 15(D)

(Sheet 2 of 3)

```
GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q

        1251        1260        1269        1278        1287        1296
GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C

        1305        1314        1323        1332        1341        1350
AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T

        1359        1368        1377        1386        1395        1404
TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C

        1413        1422        1431        1440        1449        1458
GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P

        1467        1476        1485        1494        1503        1512
GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L

        1521        1530        1539        1548        1557
GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 15(D)
(Sheet 3 of 3)

pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 346 a 468 c 434 g 312 t
ORIGIN

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

Fig. 16(A)

```
LOCUS       FDDNASE104    1560 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<793..1560)
                     /note="1 to 1560 of PAS104.dna [Split]"
     frag            721..792
                     /note="1 to 72 of 104linker"
     frag            join(721..>774,<776..792)
                     /note="1 to 72 of 103linker [Split]"
     frag            join(721..>771,<772..>774,<776..792)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      346 A    467 C    434 G    313 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
//
```

Fig. 16(B)

```
                9                  18                  27                  36                  45                  54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63                  72                  81                  90                  99                 108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117                 126                 135                 144                 153                 162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171                 180                 189                 198                 207                 216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225                 234                 243                 252                 261                 270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279                 288                 297                 306                 315                 324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333                 342                 351                 360                 369                 378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387                 396                 405                 414                 423                 432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441                 450                 459                 468                 477                 486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495                 504                 513                 522                 531                 540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549                 558                 567                 576                 585                 594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 16(C)

(Sheet 1 of 3)

```
          603                 612                 621                 630                 639                 648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657                 666                 675                 684                 693                 702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711                 720                 729                 738                 747                 756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   C   V   E   C   P   P

          765                 774                 783                 792                 801                 810
TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   A   P   E   G   R   L   K   I   A   A   F   N   I   Q   T   F

          819                 828                 837                 846                 855                 864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   E   T   K   M   S   N   A   T   L   V   S   Y   I   V   Q   I   L

          873                 882                 891                 900                 909                 918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   Y   D   I   A   L   V   Q   E   V   R   D   S   H   L   T   A

          927                 936                 945                 954                 963                 972
GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   K   L   L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y

          981                 990                 999                1008                1017                1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   V   S   E   P   L   G   R   N   S   Y   K   E   R   Y   L   F   V

         1035                1044                1053                1062                1071                1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   R   P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C

         1089                1098                1107                1116                1125                1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   P   C   G   N   D   T   F   N   R   E   P   A   I   V   R   F   F

         1143                1152                1161                1170                1179                1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   F   T   E   V   R   E   F   A   I   V   P   L   H   A   A   P

         1197                1206                1215                1224                1233                1242
```

Fig. 16(C)

(Sheet 2 of 3)

```
GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q

       1251        1260        1269        1278        1287        1296
GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C

       1305        1314        1323        1332        1341        1350
AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T

       1359        1368        1377        1386        1395        1404
TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C

       1413        1422        1431        1440        1449        1458
GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P

       1467        1476        1485        1494        1503        1512
GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L

       1521        1530        1539        1548        1557
GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   *
```

Fig. 16(C)
(Sheet 3 of 3)

pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 353 a 473 c 442 g 310 t
ORIGIN

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA
```

//

NLS

Fig. 17(A)

```
LOCUS       FDDNASE105   1578 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<781..1578)
                     /note="1 to 1578 of PAS105.dna [Split]"
     frag            721..780
                     /note="1 to 60 of 101/105linker"
     frag            join(721..>735,<736..>759,<760..>780)
                     /note="1 to 80 of 102linker [Split]"
BASE COUNT      353 A    471 C    443 G    311 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
     1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
     1561 AAGAAGCGCA AGGTTTGA
//
```

Fig. 17(B)

```
LOCUS       FDDNASE105    1587 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1587
                     /note="1 to 1578 of FdDNase105correct"
     frag            join(10..>729,<790..1587)
                     /note="1 to 1578 of PAS105.dna [Split]"
     frag            730..789
                     /note="1 to 60 of 101/105linker"
     frag            join(730..>744,<745..>768,<769..>789)
                     /note="1 to 80 of 102linker [Split]"
BASE COUNT      354 A    477 C    445 G    311 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
     1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
     1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
     1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
     1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
     1561 GGACCCAAAA AGAAGCGCAA GGTTTGA
//
```

Fig. 17(C)

```
                9          18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99         108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 17(D)

(Sheet 1 of 3)

```
          603             612             621             630             639             648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657             666             675             684             693             702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711             720             729             738             747             756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   P   P   C   P   A   P

          765             774             783             792             801             810
GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   G   L   K   I   A   A   F   N   I   Q   T   F   G   E   T   K

          819             828             837             846             855             864
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   S   N   A   T   L   V   S   Y   I   V   Q   I   L   S   R   Y   D

          873             882             891             900             909             918
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   L   V   Q   E   V   R   D   S   H   L   T   A   V   G   K   L

          927             936             945             954             963             972
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y   V   V   S   E

          981             990             999            1008            1017            1026
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   L   G   R   N   S   Y   K   E   R   Y   L   F   V   Y   R   P   D

         1035            1044            1053            1062            1071            1080
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C   E   P   C   G

         1089            1098            1107            1116            1125            1134
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   T   F   N   R   E   P   A   I   V   R   F   F   S   R   F   T

         1143            1152            1161            1170            1179            1188
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   V   R   E   F   A   I   V   P   L   H   A   A   P   G   D   A   V

         1197            1206            1215            1224            1233            1242
```

Fig. 17(D)

(Sheet 2 of 3)

```
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q   E   K   W   G

       1251        1260        1269        1278        1287        1296
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   D   V   M   L   M   G   D   F   N   A   G   C   S   Y   V   R

       1305        1314        1323        1332        1341        1350
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   Q   W   S   S   I   R   L   W   T   S   P   T   F   Q   W   L

       1359        1368        1377        1386        1395        1404
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   P   D   S   A   D   T   T   A   T   P   T   H   C   A   Y   D   R

       1413        1422        1431        1440        1449        1458
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   V   V   A   G   M   L   L   R   G   A   V   V   P   D   S   A   L

       1467        1476        1485        1494        1503        1512
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L   A   Q   A   I

       1521        1530        1539        1548        1557        1566
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   D   H   Y   P   V   E   V   M   L   K   G   G   G   P   K   K   K

       1575
CGC AAG GTT TGA 3'
--- --- --- ---
 R   K   V   *
```

Fig. 17(D)
(Sheet 3 of 3)

pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(pAS106)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 355 a 475 c 452 g 314 t
ORIGIN

```
   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA
```

//

NLS

Fig. 18(A)

```
LOCUS       FDDNASE106   1596 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<799..1596)
                     /note="1 to 1596 of PAS106.dna [Split]"
     frag            721..798
                     /note="1 to 78 of 102/106linker"
BASE COUNT      355 A    474 C    452 G    315 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA
//
```

Fig. 18(B)

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LOCUS       FDDNASE106    1605 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
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                     /note="1 to 1596 of FdDNase106correct"
     frag            join(10..>729,<808..1605)
                     /note="1 to 1596 of PAS106.dna [Split]"
     frag            730..807
                     /note="1 to 78 of 102/106linker"
BASE COUNT      356 A    480 C    454 G    315 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
     1561 GTGATGCTGA AGGGGGGCGG ACCCAAAAAG AAGCGCAAGG TTTGA
//
```

Fig. 18(C)

```
                9                  18                  27                  36                  45                  54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63                  72                  81                  90                  99                 108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117                 126                 135                 144                 153                 162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171                 180                 189                 198                 207                 216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225                 234                 243                 252                 261                 270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279                 288                 297                 306                 315                 324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333                 342                 351                 360                 369                 378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387                 396                 405                 414                 423                 432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441                 450                 459                 468                 477                 486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495                 504                 513                 522                 531                 540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549                 558                 567                 576                 585                 594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```

Fig. 18(D)

(Sheet 1 of 3)

```
          603                 612                 621                 630                 639                 648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657                 666                 675                 684                 693                 702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711                 720                 729                 738                 747                 756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   C   V   E   C   P   P

          765                 774                 783                 792                 801                 810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   A   P   E   G   S   G   G   L   K   I   A   A   F   N   I   Q

          819                 828                 837                 846                 855                 864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   F   G   E   T   K   M   S   N   A   T   L   V   S   Y   I   V   Q

          873                 882                 891                 900                 909                 918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   L   S   R   Y   D   I   A   L   V   Q   E   V   R   D   S   H   L

          927                 936                 945                 954                 963                 972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   A   V   G   K   L   L   D   N   L   N   Q   D   A   P   D   T   Y

          981                 990                 999                1008                1017                1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   Y   V   V   S   E   P   L   G   R   N   S   Y   K   E   R   Y   L

         1035                1044                1053                1062                1071                1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   V   Y   R   P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D

         1089                1098                1107                1116                1125                1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   C   E   P   C   G   N   D   T   F   N   R   E   P   A   I   V   R

         1143                1152                1161                1170                1179                1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   F   S   R   F   T   E   V   R   E   F   A   I   V   P   L   H   A

         1197                1206                1215                1224                1233                1242
```


Fig. 18(D)

(Sheet 2 of 3)

```
GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   P   G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D

       1251        1260        1269        1278        1287        1296
GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   Q   E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A

       1305        1314        1323        1332        1341        1350
GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   C   S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S

       1359        1368        1377        1386        1395        1404
CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   T   F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T

       1413        1422        1431        1440        1449        1458
CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   C   A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V

       1467        1476        1485        1494        1503        1512
GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   P   D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D

       1521        1530        1539        1548        1557        1566
CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   L   A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   G

         1575        1584        1593
GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3'
--- --- --- --- --- --- --- --- --- ---
 G   G   P   K   K   K   R   K   V   *
```

Fig. 18(D)

(Sheet 3 of 3)

pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(pAS107)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 448 g 314 t
ORIGIN

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   1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA
//
```

NLS

Fig. 19(A)

```
LOCUS       FDDNASE107   1590 BP SS-DNA              SYN       25-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            join(1..>720,<793..1590)
                     /note="1 to 1590 of PAS107.dna [Split]"
     frag            721..792
                     /note="1 to 72 of 103/107linker"
     frag            join(721..>771,<772..792)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      354 A    473 C    448 G    315 T      0 OTHER
ORIGIN      -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
     1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA
//
```

Fig. 19(B)

```
LOCUS       FDDNASE107    1599 BP SS-DNA              SYN       29-AUG-2000
DEFINITION  -
ACCESSION   -
KEYWORDS    -
SOURCE      -
FEATURES             Location/Qualifiers
     frag            10..1599
                     /note="1 to 1590 of FdDNase107correct"
     frag            join(10..>729,<802..1599)
                     /note="1 to 1590 of PAS107.dna [Split]"
     frag            730..801
                     /note="1 to 72 of 103/107linker"
     frag            join(730..>780,<781..801)
                     /note="1 to 78 of 102linker [Split]"
BASE COUNT      355 A    479 C    450 G    315 T      0 OTHER
ORIGIN      -
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
     1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA
//
```

Fig. 19(C)

```
                9           18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   G   W   S   C   I   I   L   F   L   V   A   T   A   T   G   V   H

               63          72          81          90          99         108
    TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S

              117         126         135         144         153         162
    GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   K   V   S   C   K   A   S   G   Y   T   F   S   A   Y   W   I   E

              171         180         189         198         207         216
    TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   V   R   Q   A   P   G   K   G   L   E   W   V   G   E   I   L   P

              225         234         243         252         261         270
    GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   S   N   N   S   R   Y   N   E   K   F   K   G   R   V   T   V   T

              279         288         297         306         315         324
    AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     R   D   T   S   T   N   T   A   Y   M   E   L   S   S   L   R   S   E

              333         342         351         360         369         378
    GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     D   T   A   V   Y   Y   C   A   R   S   Y   D   F   A   W   F   A   Y

              387         396         405         414         423         432
    TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K   G   P   S

              441         450         459         468         477         486
    GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   F   P   L   A   P   S   S   K   S   T   S   G   G   T   A   A   L

              495         504         513         522         531         540
    GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   C   L   V   K   D   Y   F   P   E   P   V   T   V   S   W   N   S

              549         558         567         576         585         594
    GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     G   A   L   T   S   G   V   H   T   F   P   A   V   L   Q   S   S   G
```


Fig. 19(D)

(Sheet 1 of 3)

```
          603             612             621             630             639             648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   Y   S   L   S   S   V   V   T   V   P   S   S   S   L   G   T   Q

          657             666             675             684             693             702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   Y   I   C   N   V   N   H   K   P   S   N   T   K   V   D   K   K

          711             720             729             738             747             756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   E   P   K   S   C   D   K   T   H   T   C   C   V   E   C   P   P

          765             774             783             792             801             810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   A   P   E   G   G   L   K   I   A   A   F   N   I   Q   T   F

          819             828             837             846             855             864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   E   T   K   M   S   N   A   T   L   V   S   Y   I   V   Q   I   L

          873             882             891             900             909             918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   Y   D   I   A   L   V   Q   E   V   R   D   S   H   L   T   A

          927             936             945             954             963             972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   G   K   L   L   D   N   L   N   Q   D   A   P   D   T   Y   H   Y

          981             990             999            1008            1017            1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   V   S   E   P   L   G   R   N   S   Y   K   E   R   Y   L   F   V

         1035            1044            1053            1062            1071            1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   R   P   D   Q   V   S   A   V   D   S   Y   Y   Y   D   D   G   C

         1089            1098            1107            1116            1125            1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   P   C   G   N   D   T   F   N   R   E   P   A   I   V   R   F   F

         1143            1152            1161            1170            1179            1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   F   T   E   V   R   E   F   A   I   V   P   L   H   A   A   P

         1197            1206            1215            1224            1233            1242
```

Fig. 19(D)

(Sheet 2 of 3)

```
GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q

       1251        1260        1269        1278        1287        1296
GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C

       1305        1314        1323        1332        1341        1350
AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T

       1359        1368        1377        1386        1395        1404
TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C

       1413        1422        1431        1440        1449        1458
GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P

       1467        1476        1485        1494        1503        1512
GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L

       1521        1530        1539        1548        1557        1566
GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   G   G   G

       1575        1584
CCC AAA AAG AAG CGC AAG GTT TGA 3'
--- --- --- --- --- --- --- ---
 P   K   K   K   R   K   V   *
```

Fig. 19(D)
(Sheet 3 of 3)

Mammalian expression of humanised HMFG1-D Nase constructs

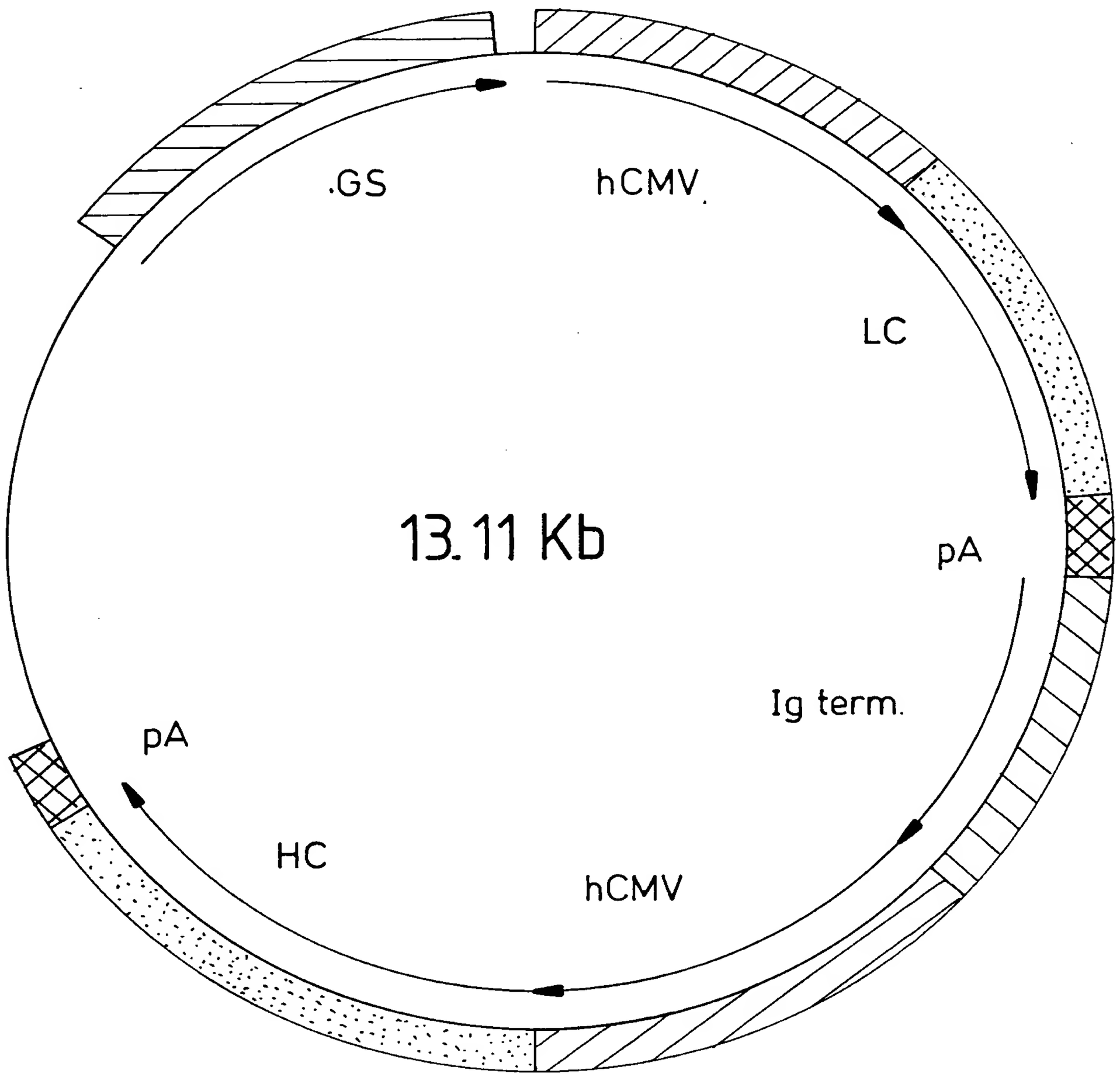
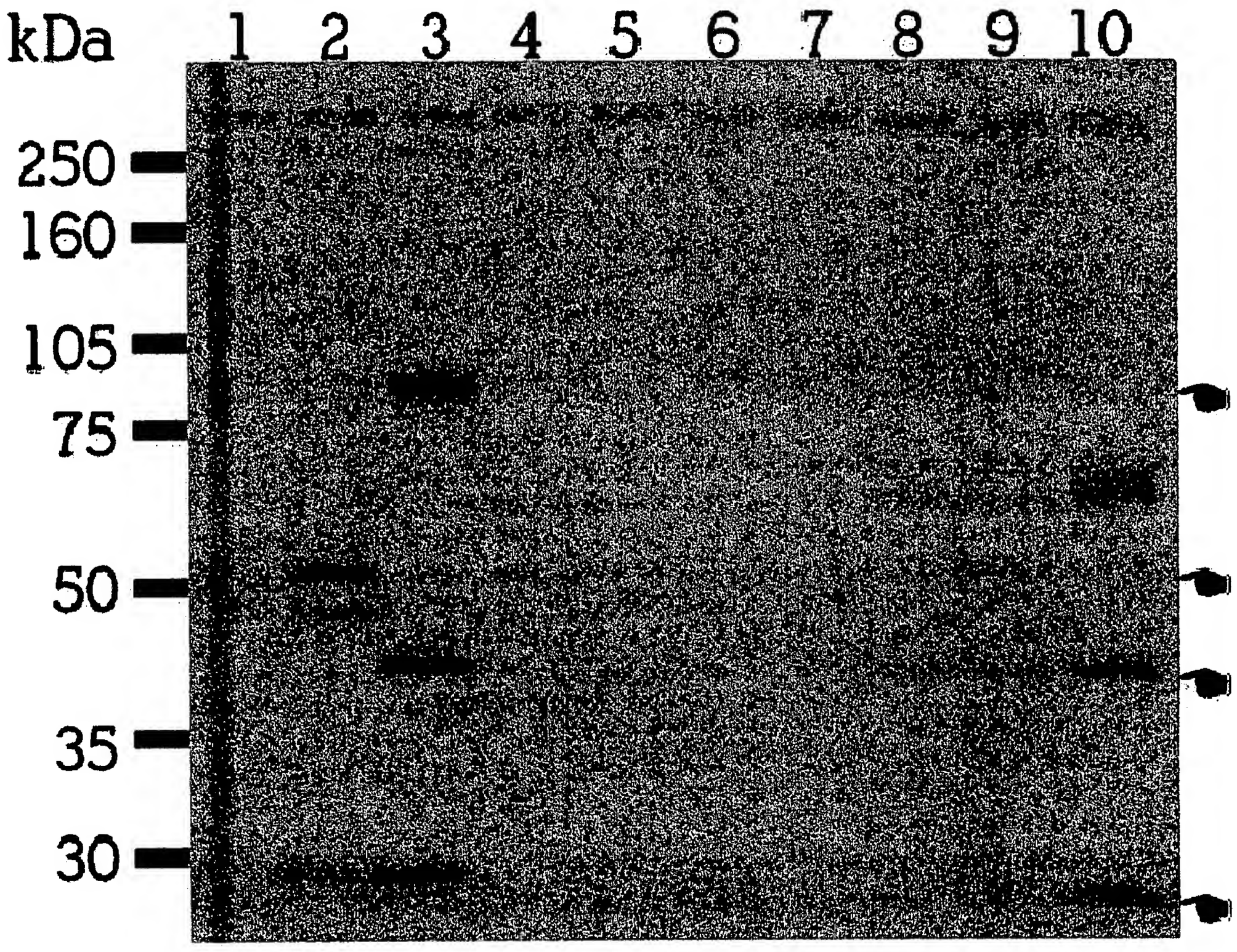


Fig. 20

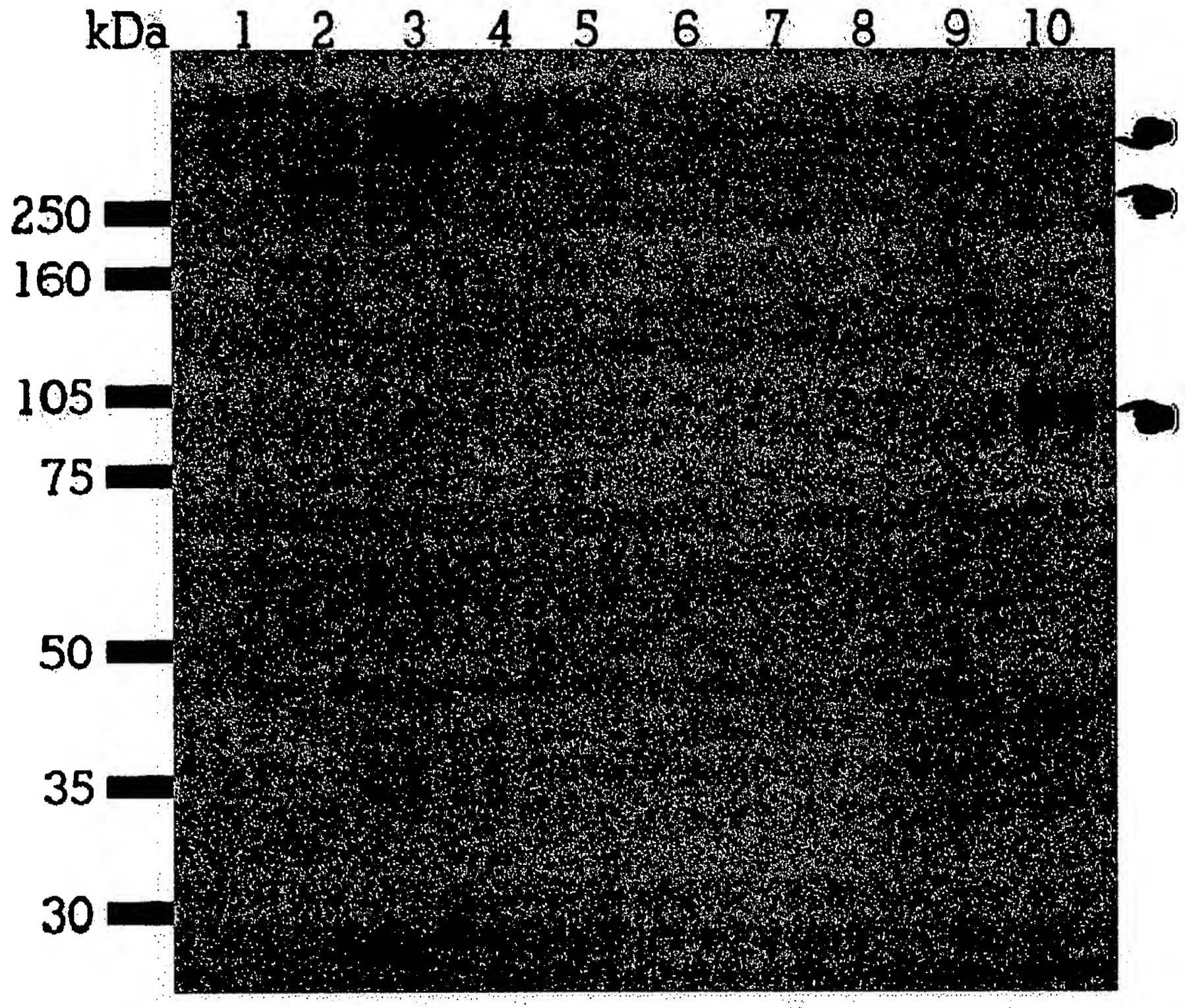
Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE reducing gel

Fig. 21(A)

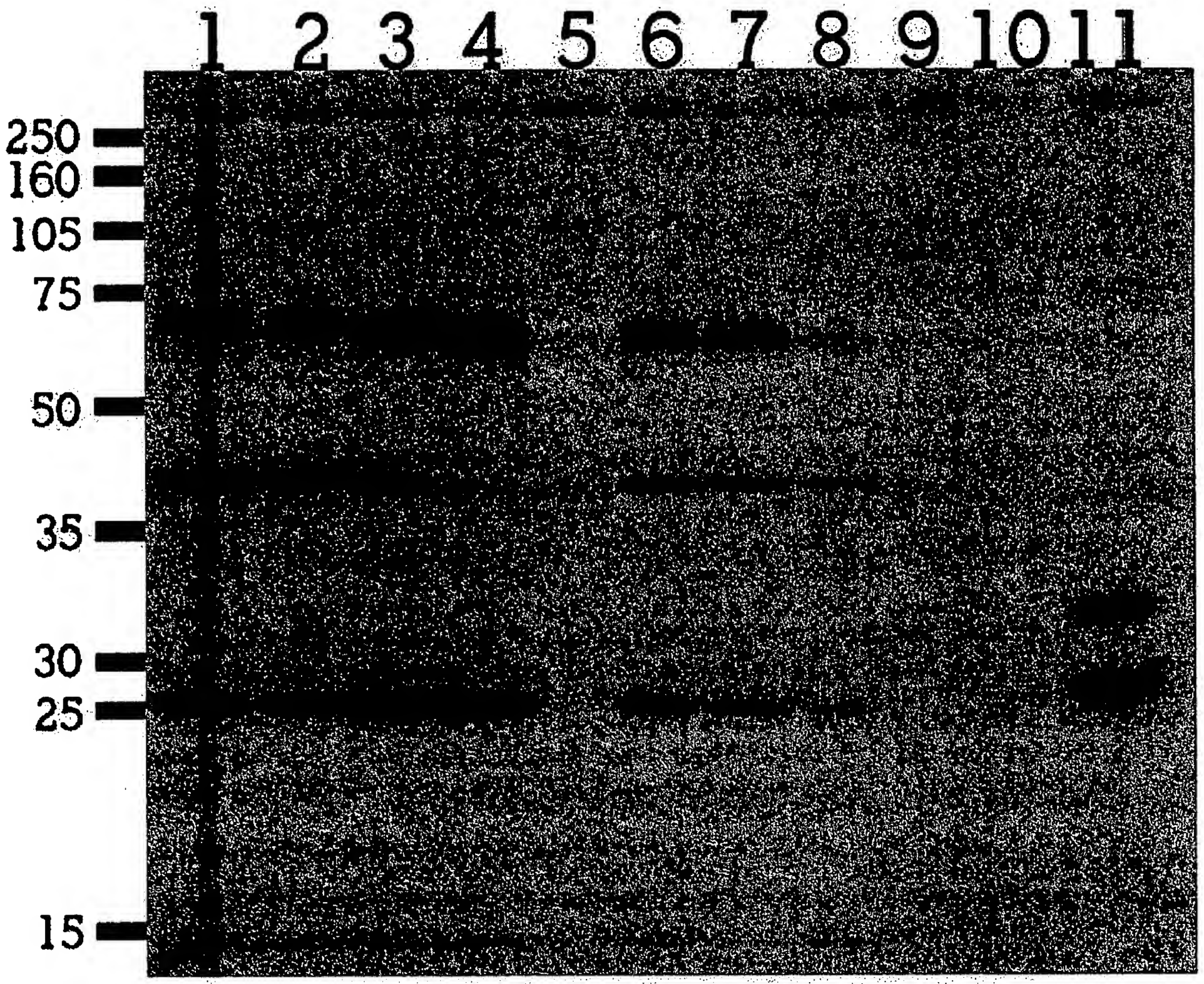
Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE non-reducing gel

Fig. 21(B)

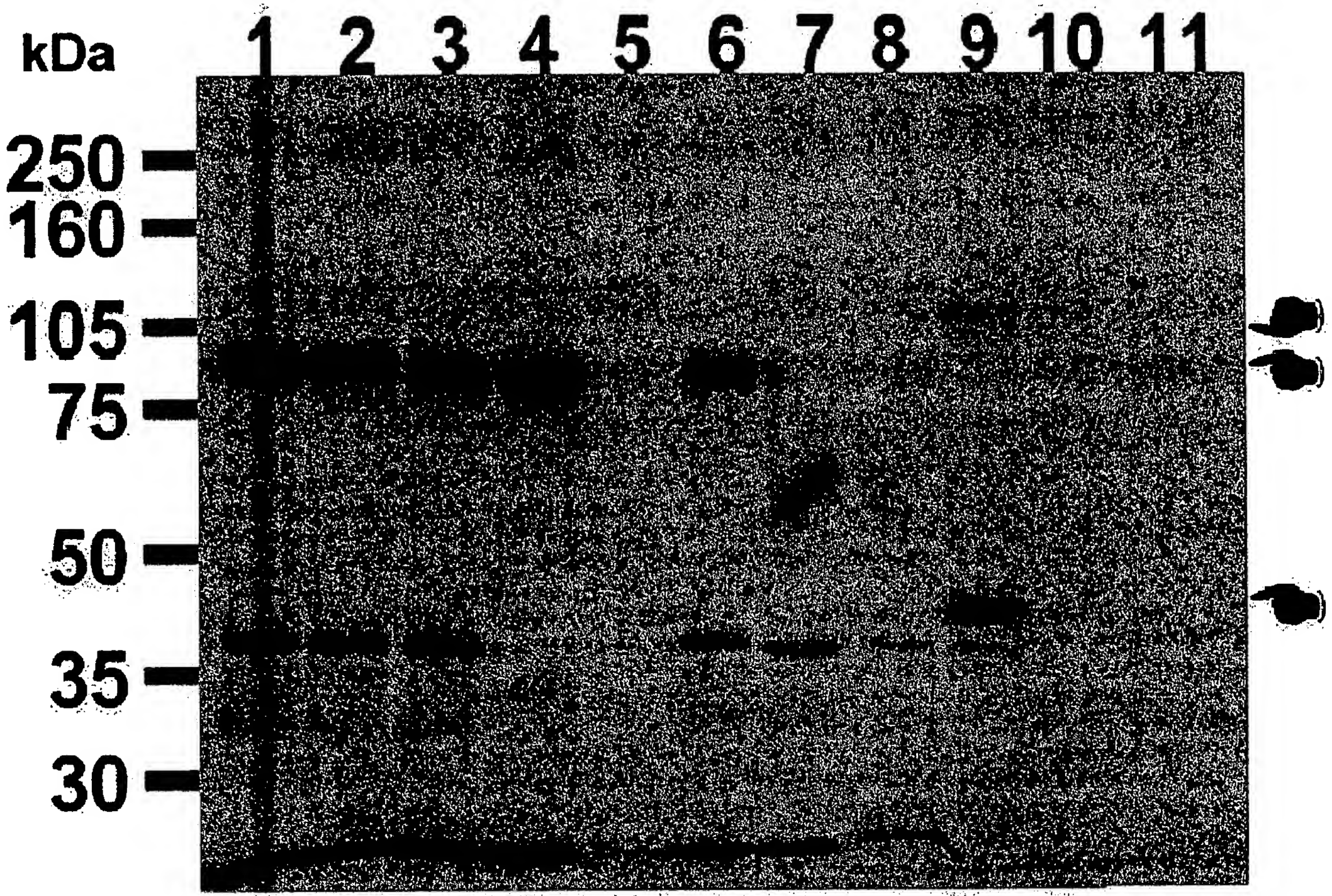
Immuno-precipitation of metabolically labelled transient transfectants



10% SDS-PAGE reducing gel

Fig. 21(C)

Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE non-reducing gel

Fig. 21(D)

Fig. 22

PDTRP binding assay standard curve (5' development)

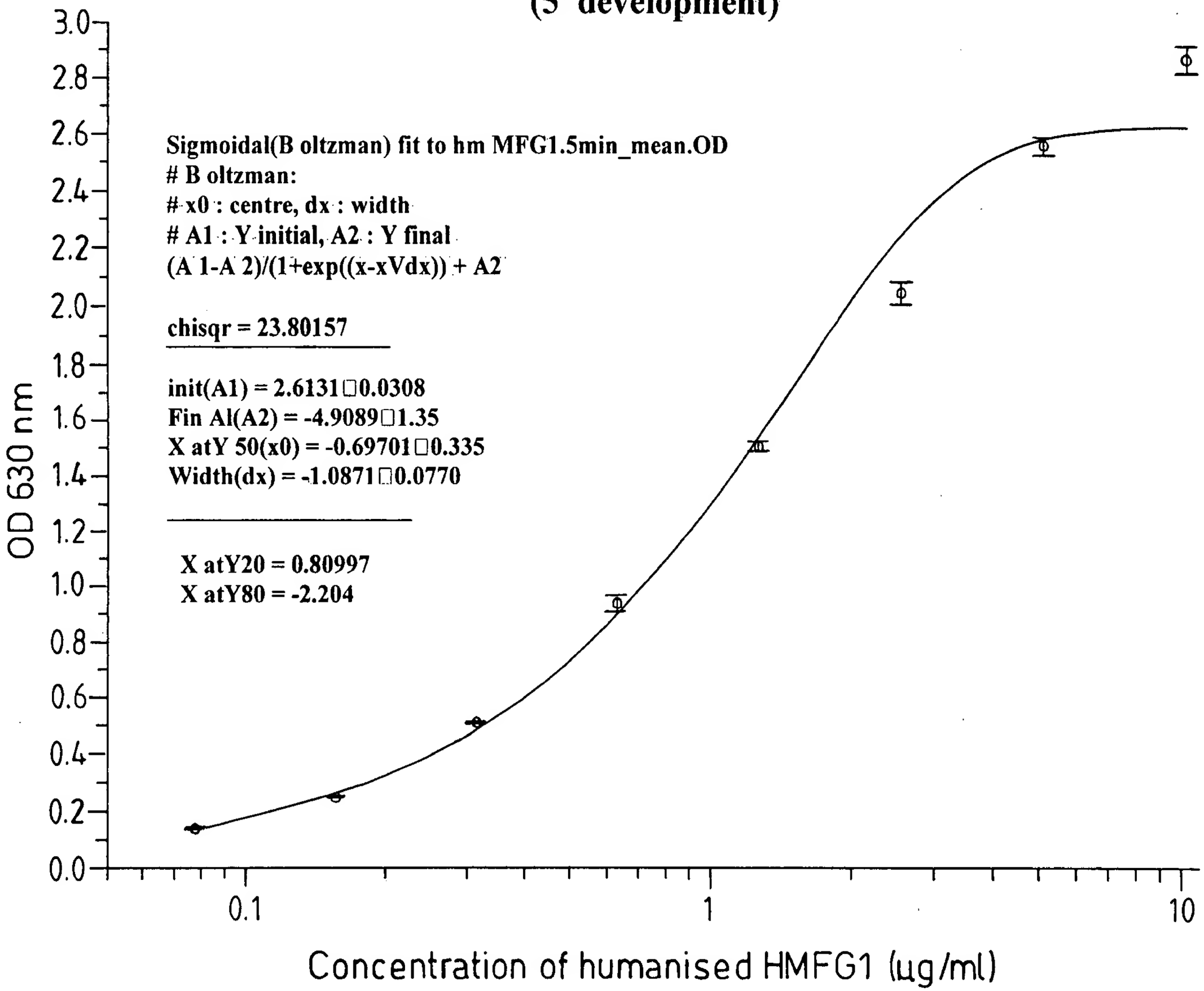
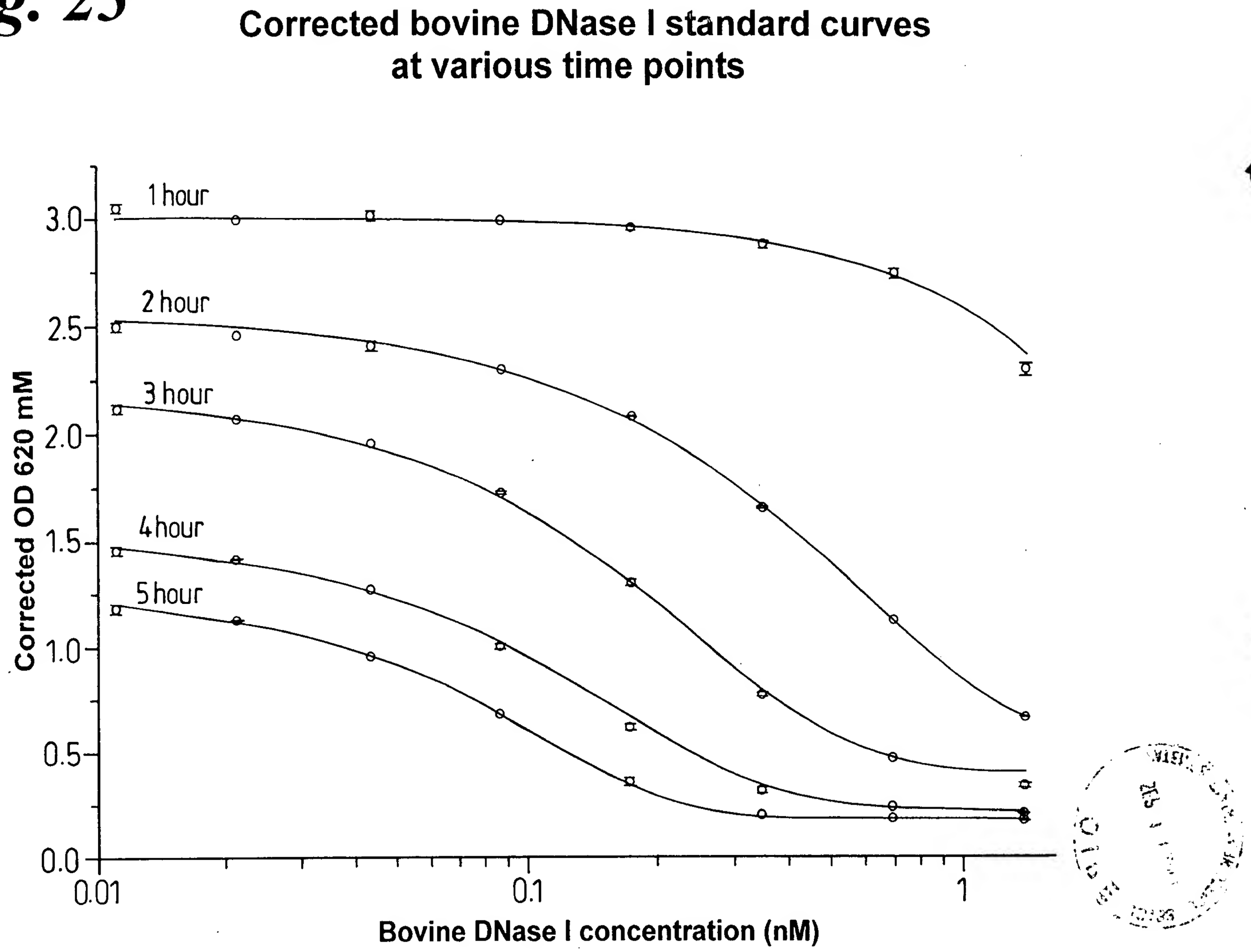


Fig. 23


Corrected bovine DNase I standard curves
at various time points
1 hour
2 hour
3 hour
4 hour
5 hour
Corrected OD 620 mM
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.01
0.1
1
Bovine DNase I concentration (nM)

Corrected DNase I activity in transiently expressed humanised human HMFG1-human DNase I constructs

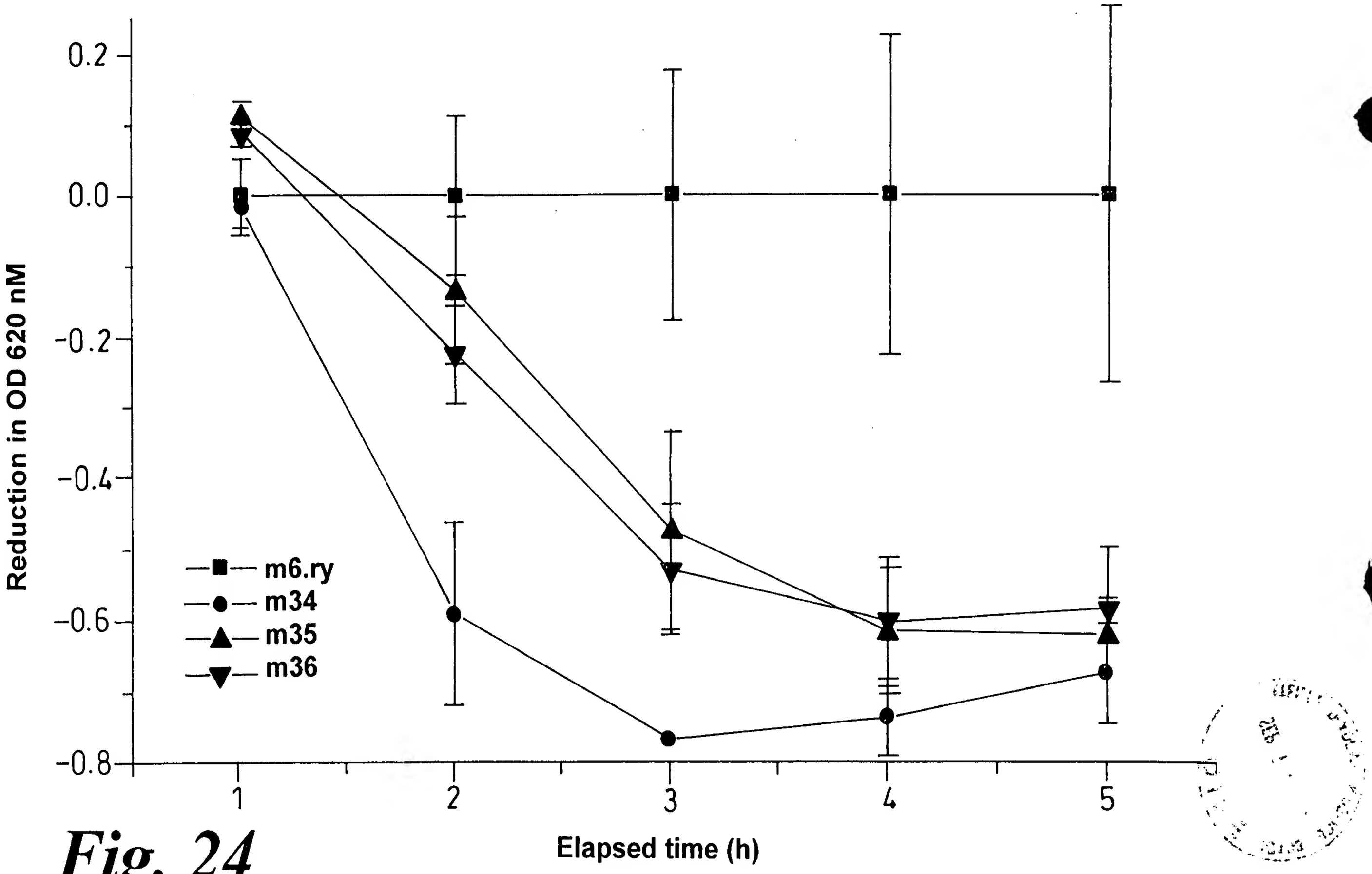


Fig. 24

Corrected DNase I activity in transiently expressed humanised HMFG1 F(ab')2-human DNase I fusions

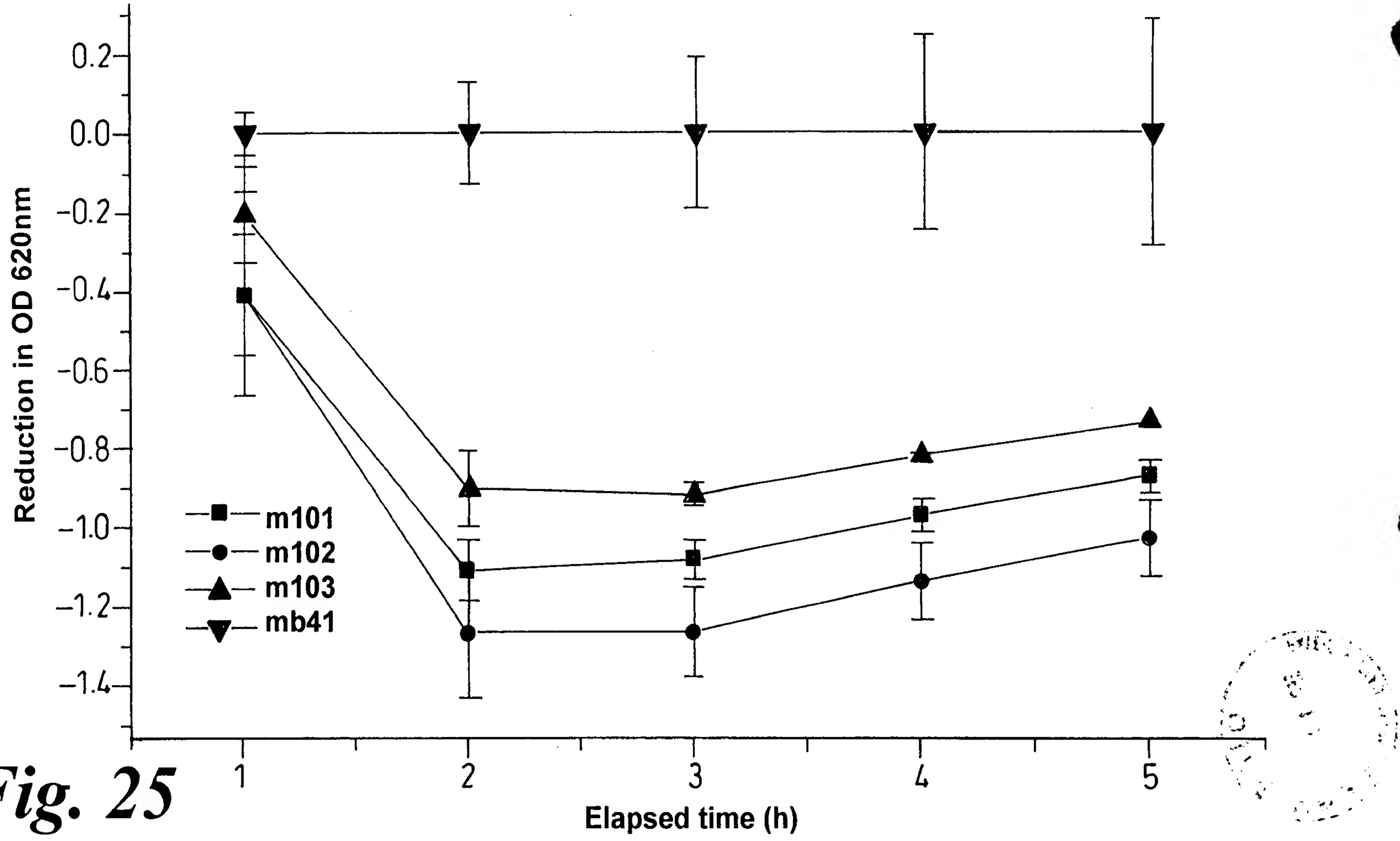


Fig. 25

Fig. 26

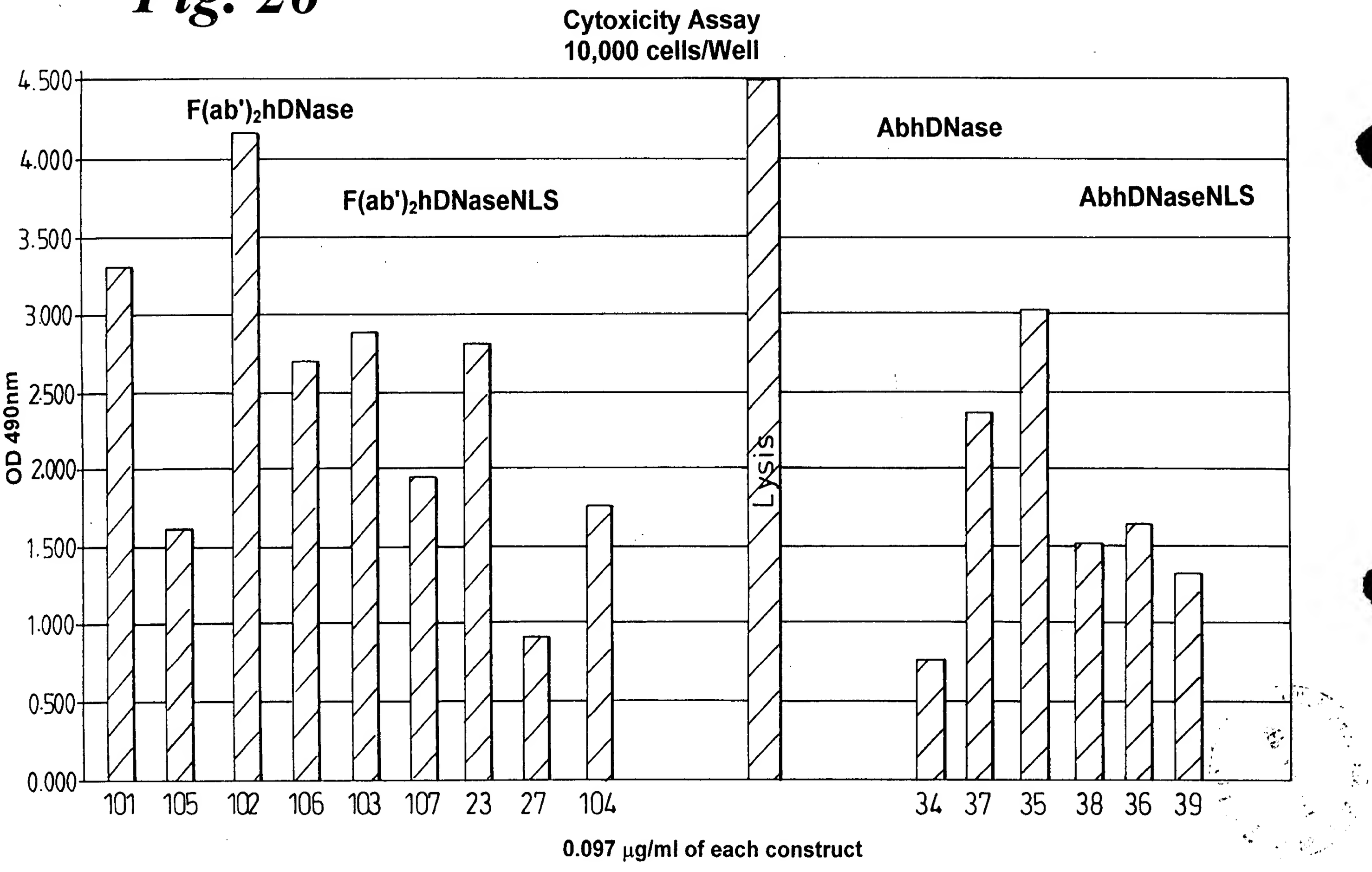
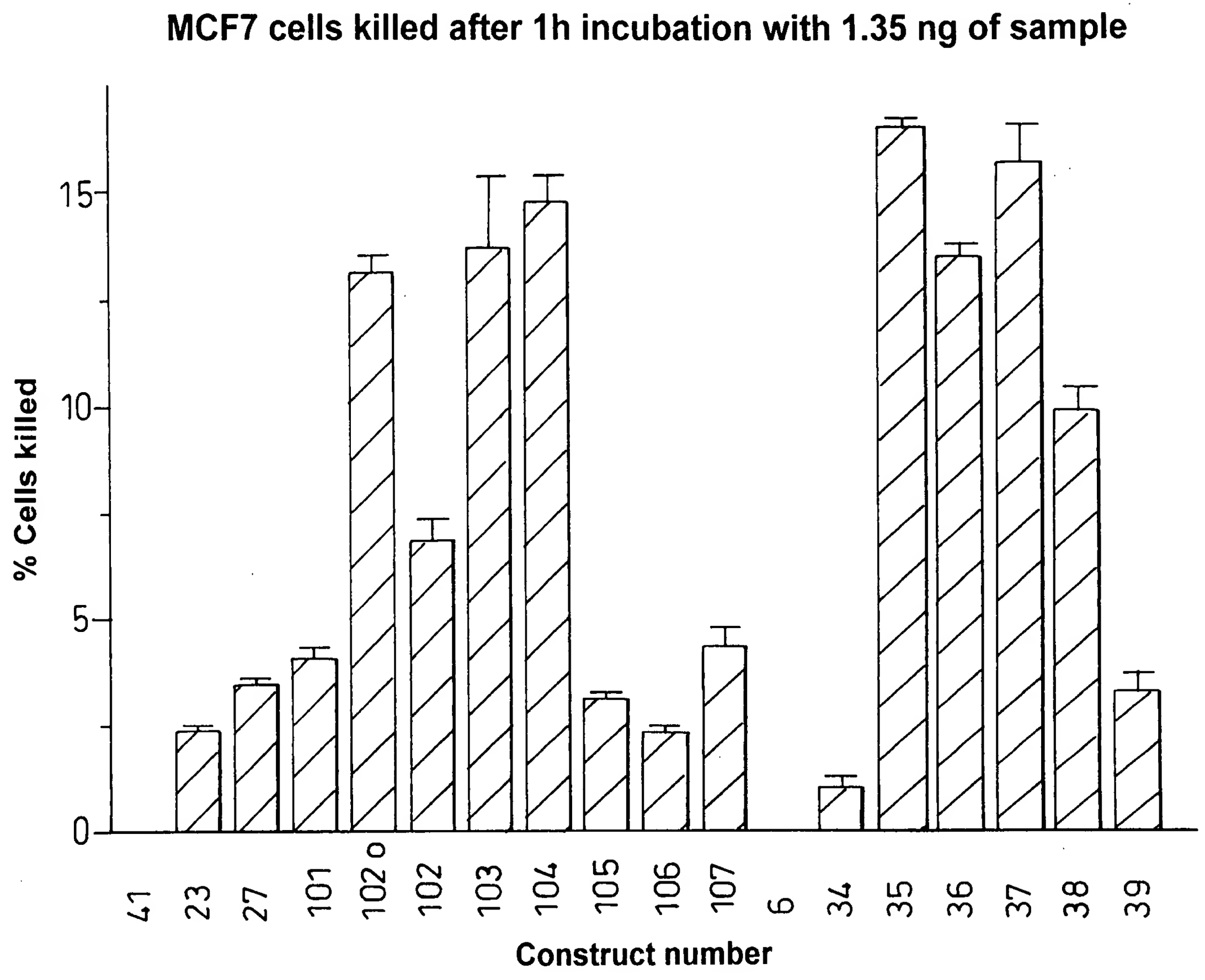

Cytoxicity Assay
10,000 cells/Well
F(ab')2hDNase
F(ab')2hDNaseNLS
AbhDNase
AbhDNaseNLS
Lysis
OD 490nm
4.500
4.000
3.500
3.000
2.500
2.000
1.500
1.000
0.500
0.000
101
105
102
106
103
107
23
27
104
34
37
35
38
36
39
0.097 µg/ml of each construct

Fig. 27


MCF7 cells killed after 1h incubation with 1.35 ng of sample
% Cells killed
0
5
10
15
41
23
27
101
102 o
102
103
104
105
106
107
6
34
35
36
37
38
39
Construct number

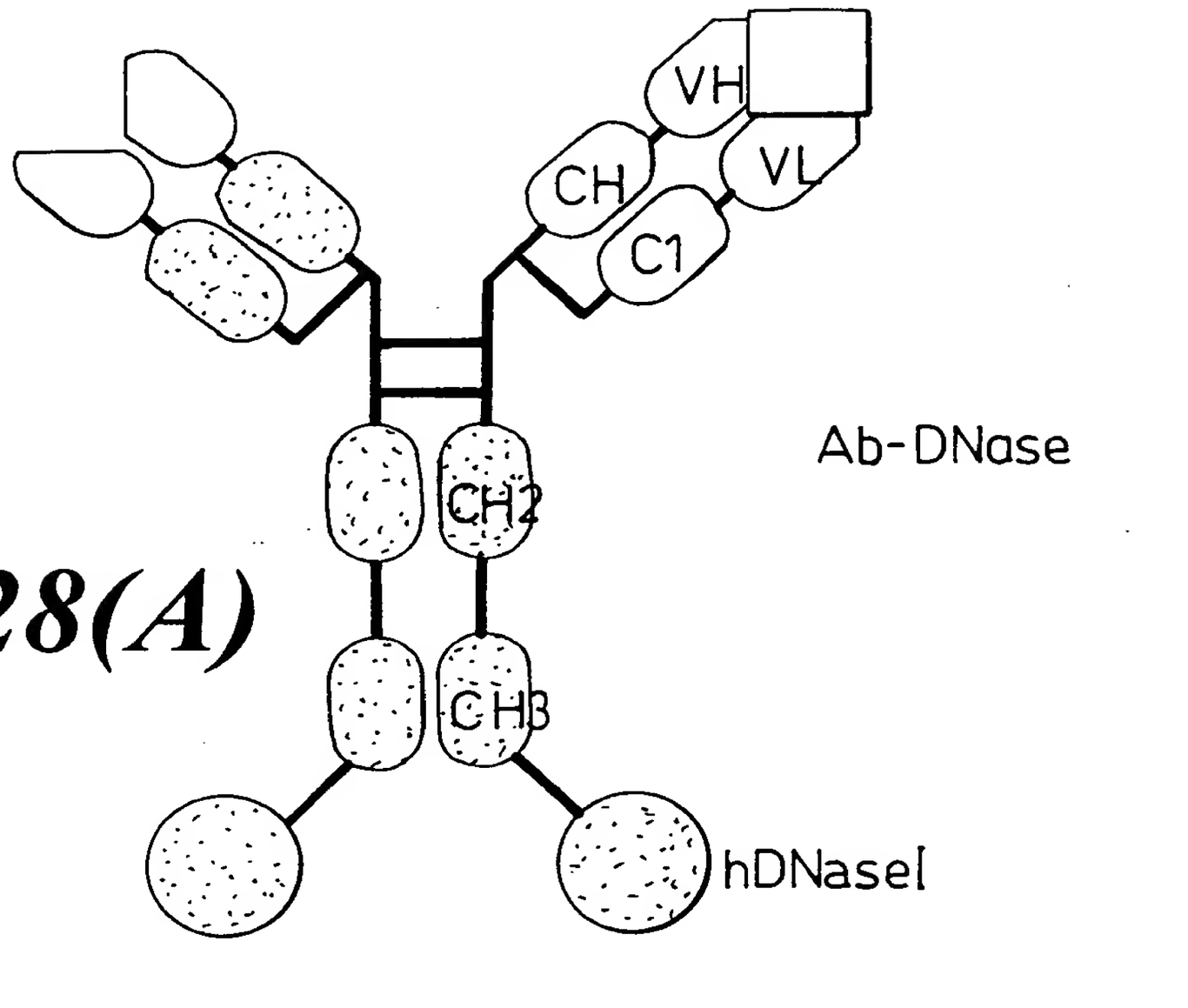


Fig. 28(A)

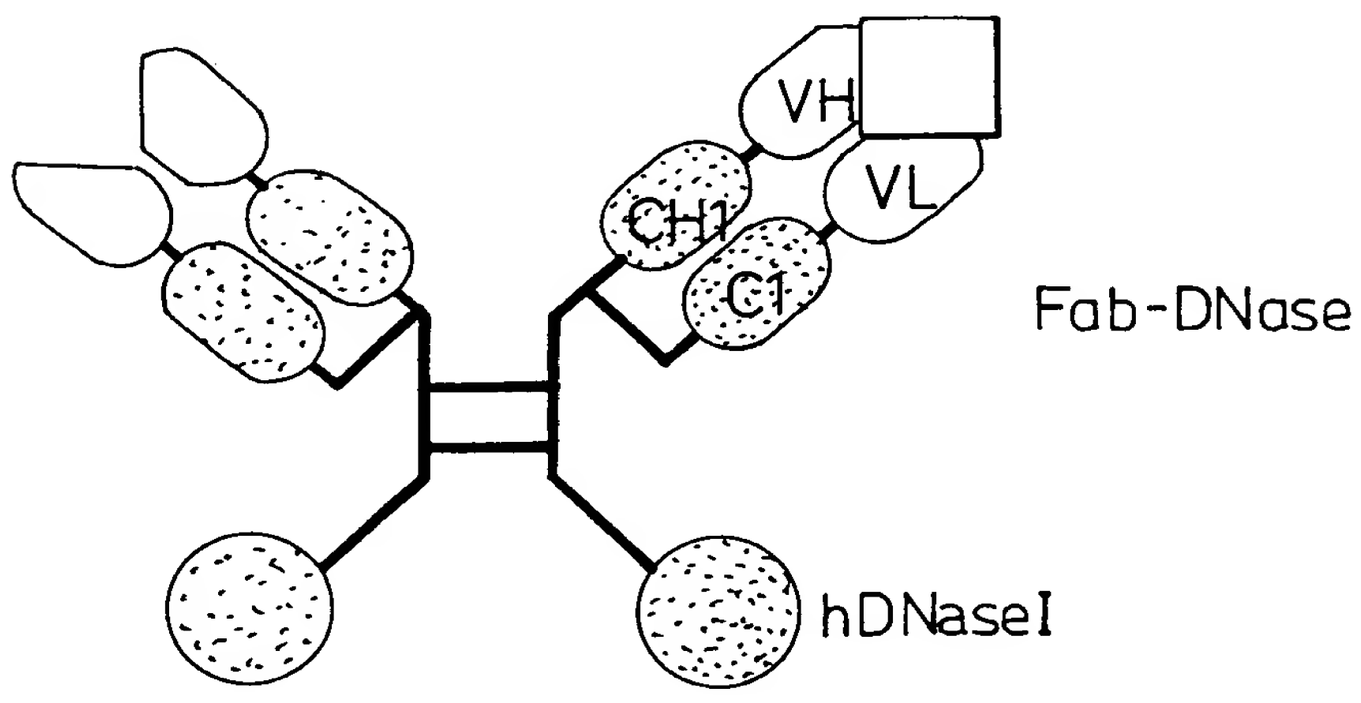
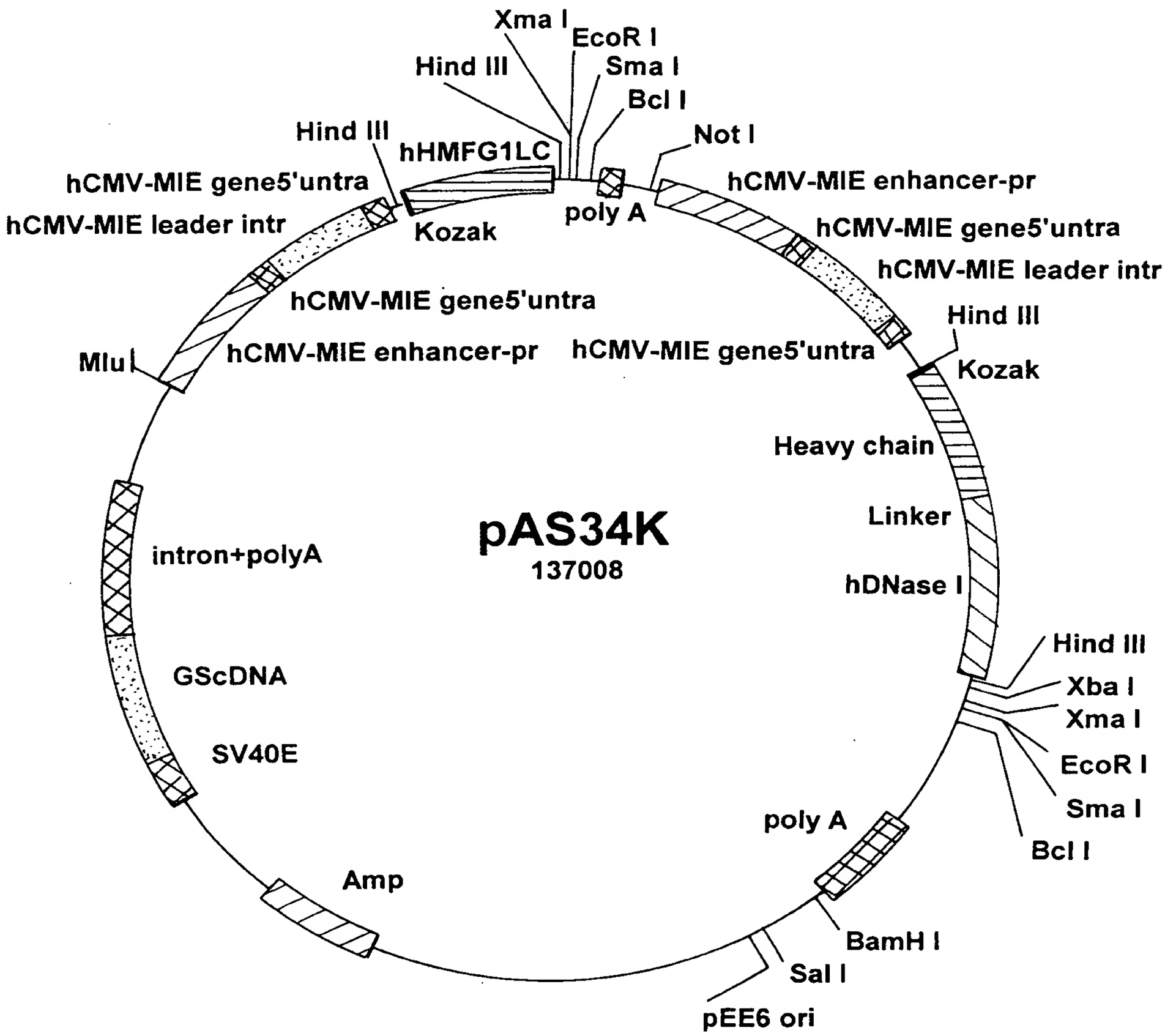
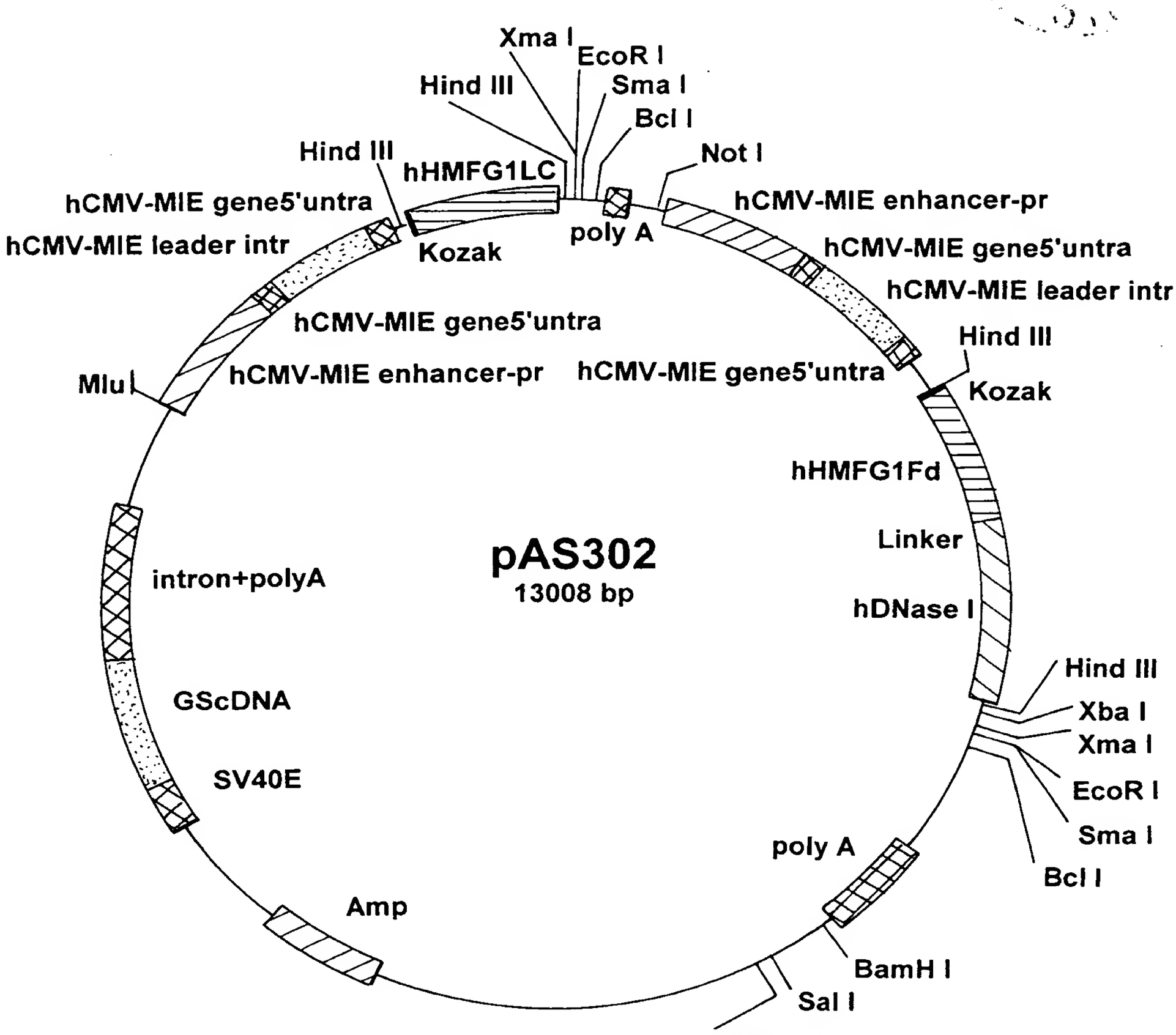


Fig. 28(B)



Ab-DNase

Fig. 29



Fab-DNase

Fig. 30

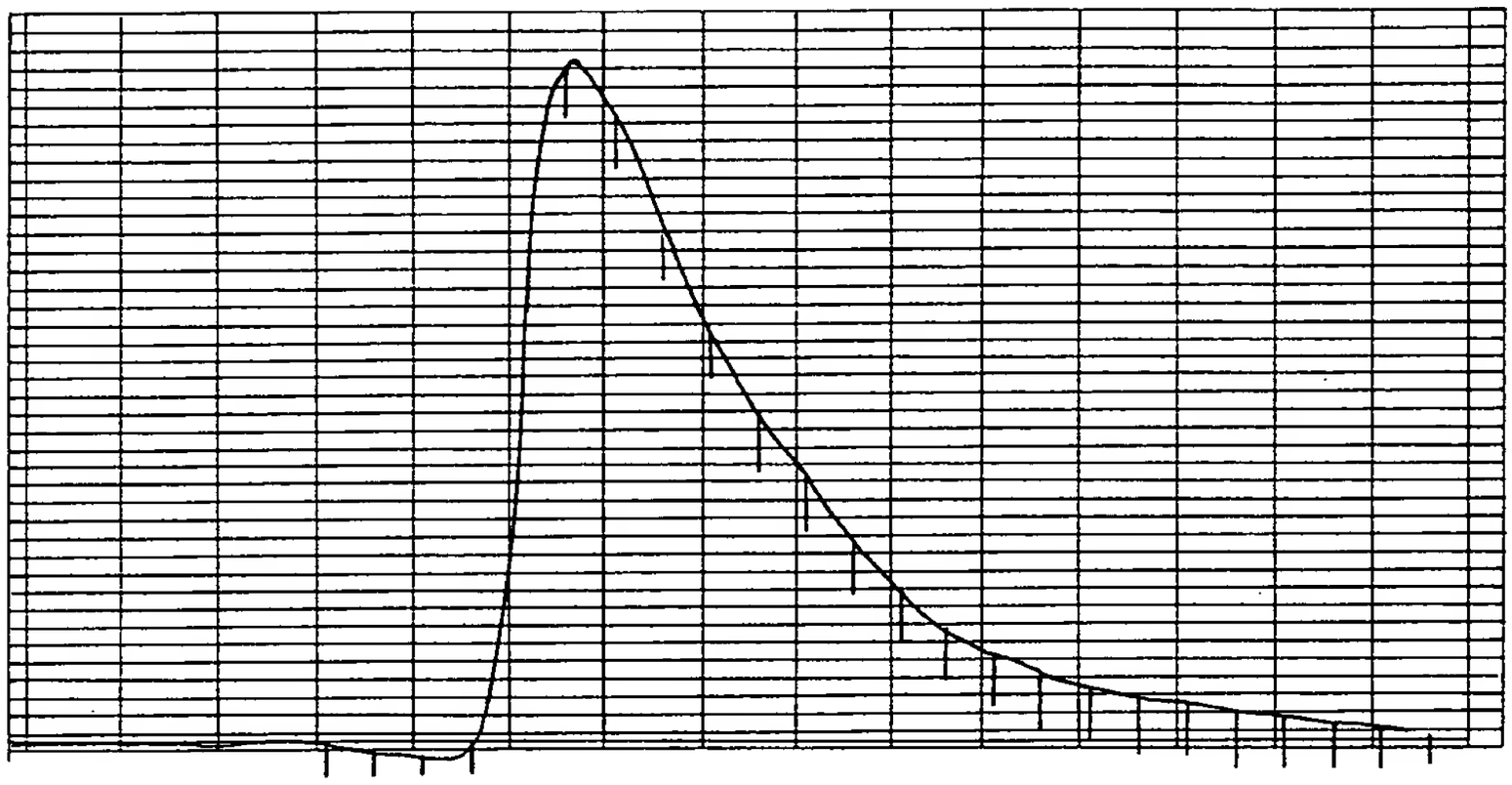


Fig. 31(A)

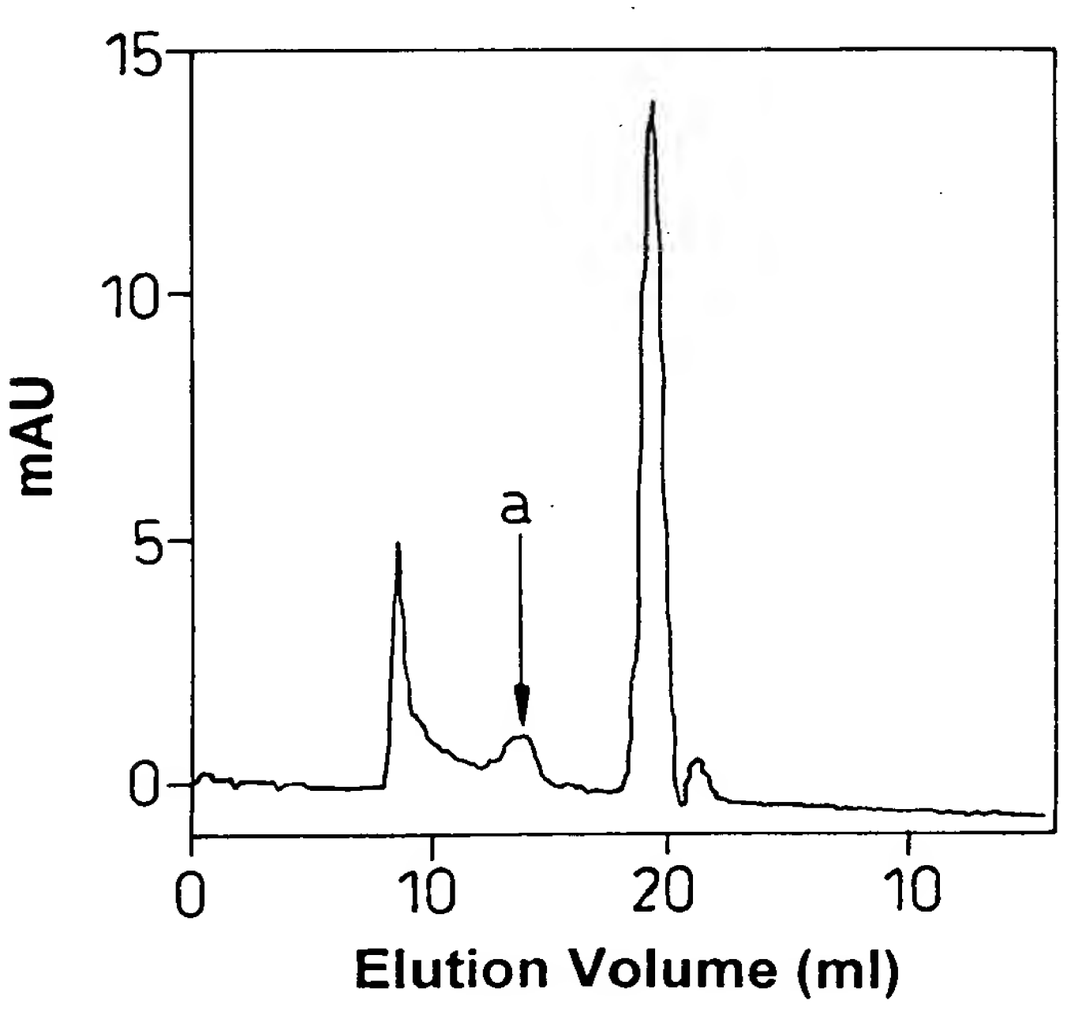


Fig. 31(B)

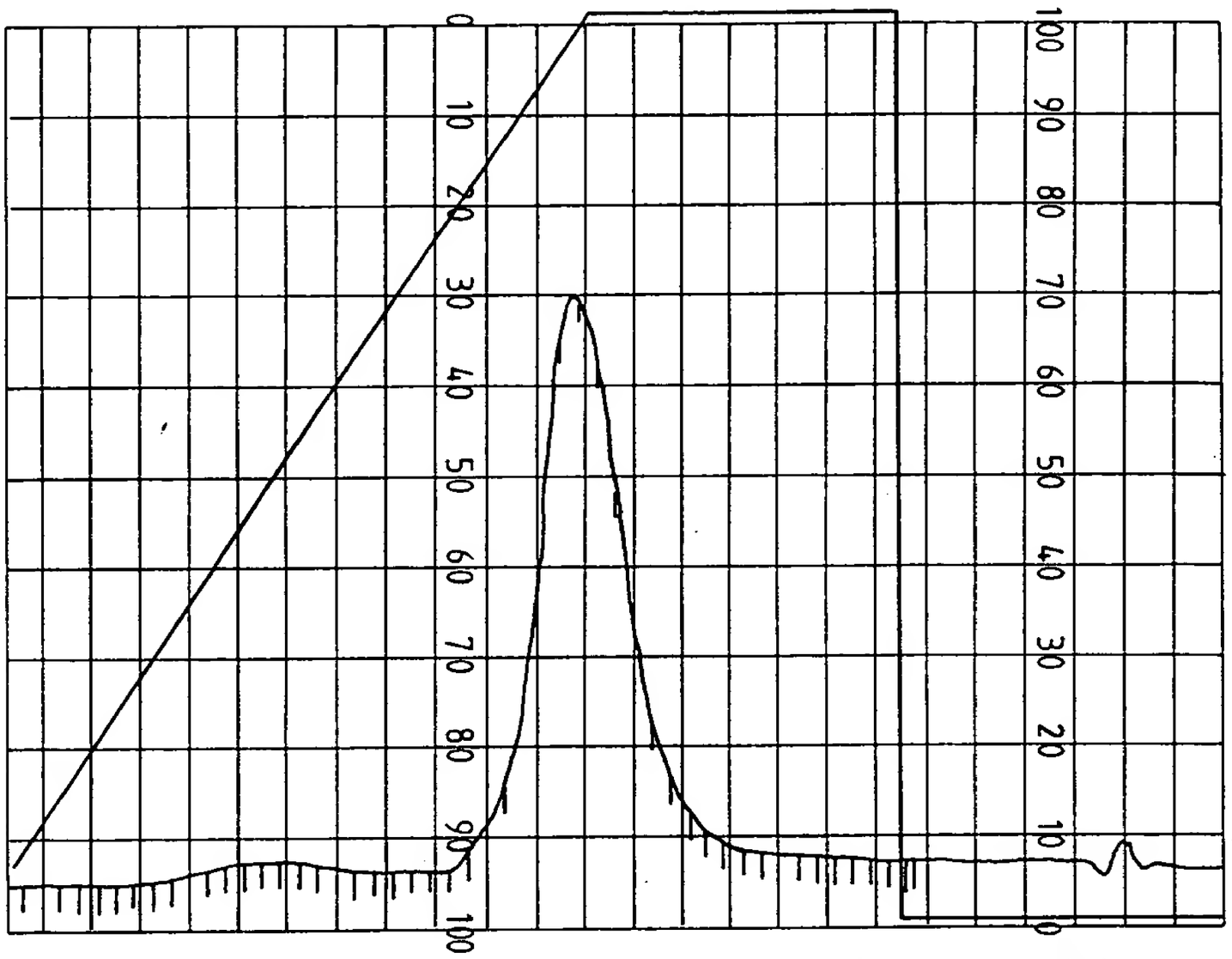


Fig. 32(A)

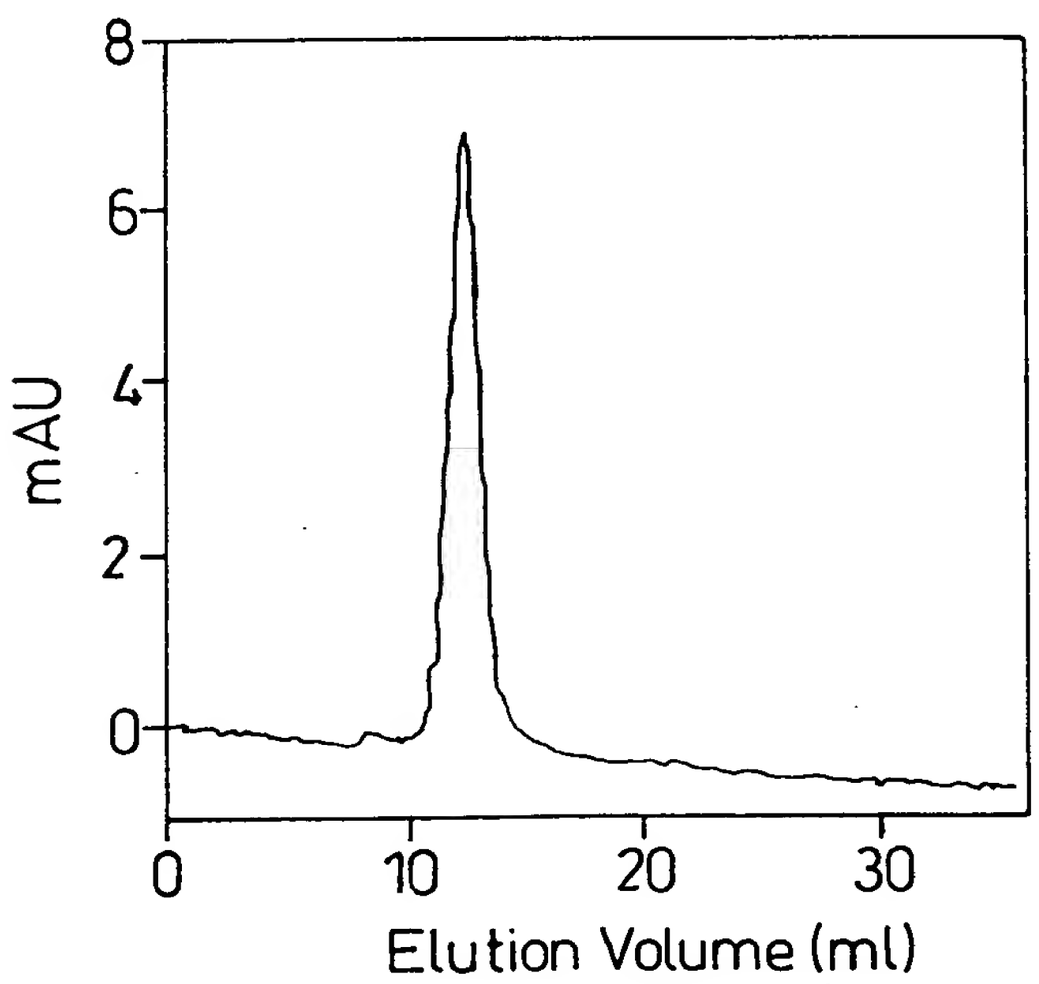


Fig. 32(B)

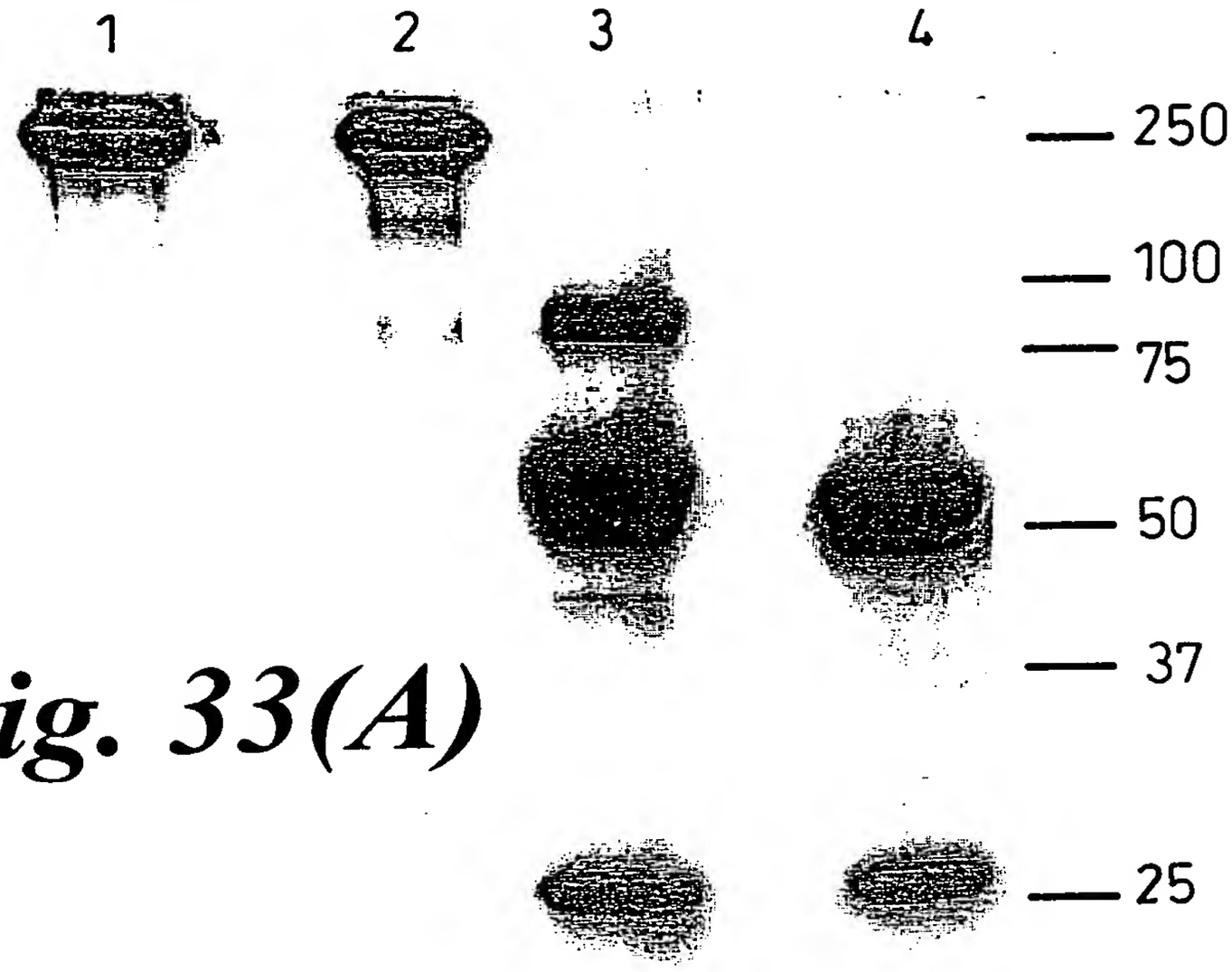


Fig. 33(A)

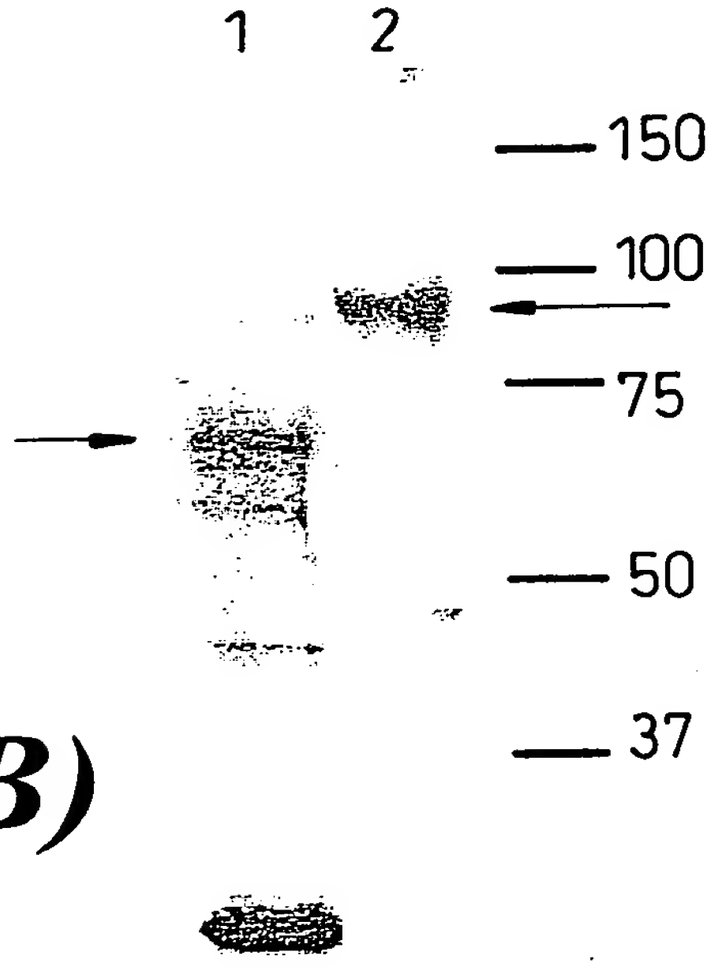


Fig. 33(B)

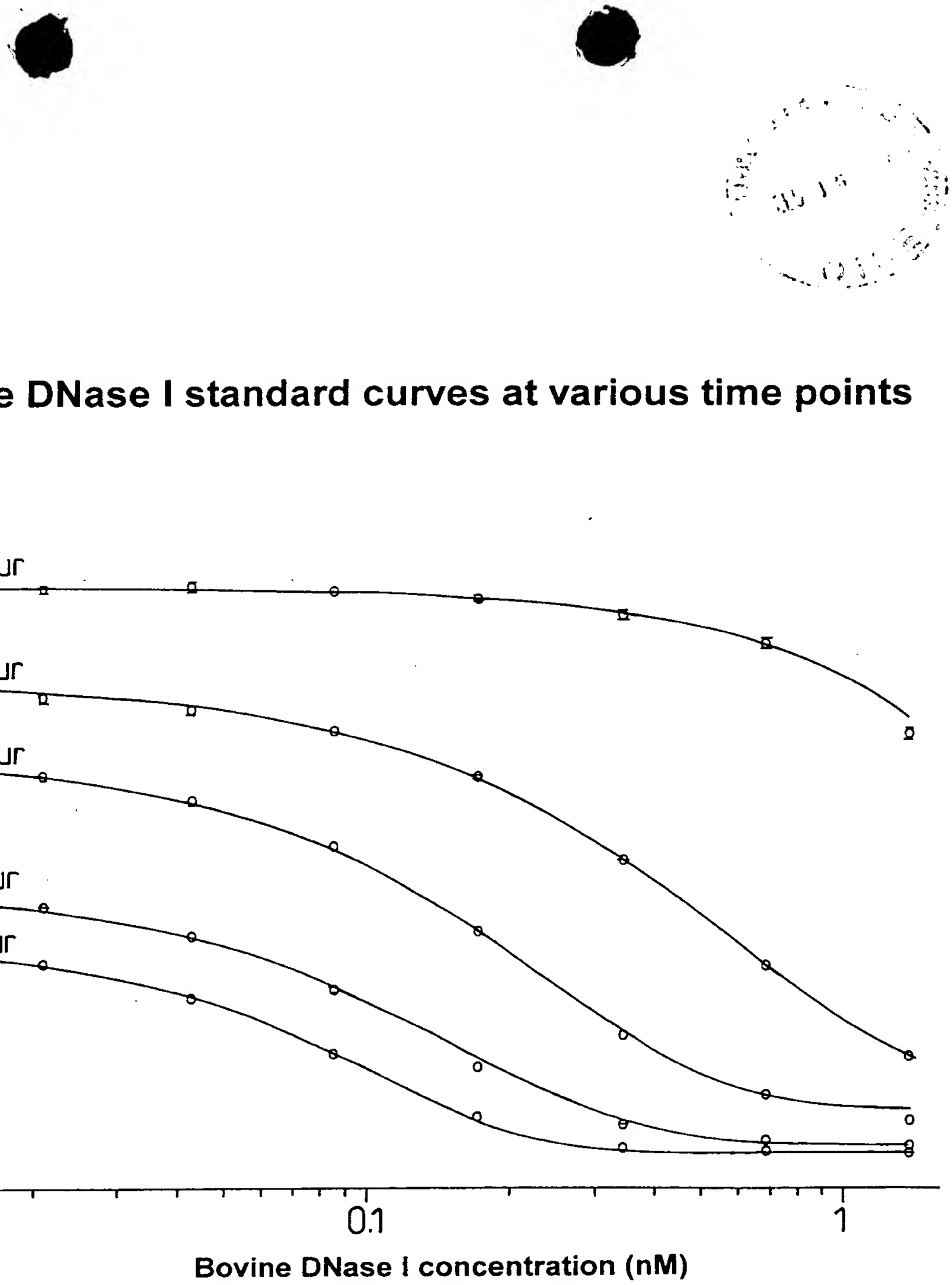

Bovine DNase I standard curves at various time points
1 hour
2 hour
3 hour
4 hour
5 hour
Corrected OD 620 nm
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.01
0.1
1
Bovine DNase I concentration (nM)

Fig. 34(A)

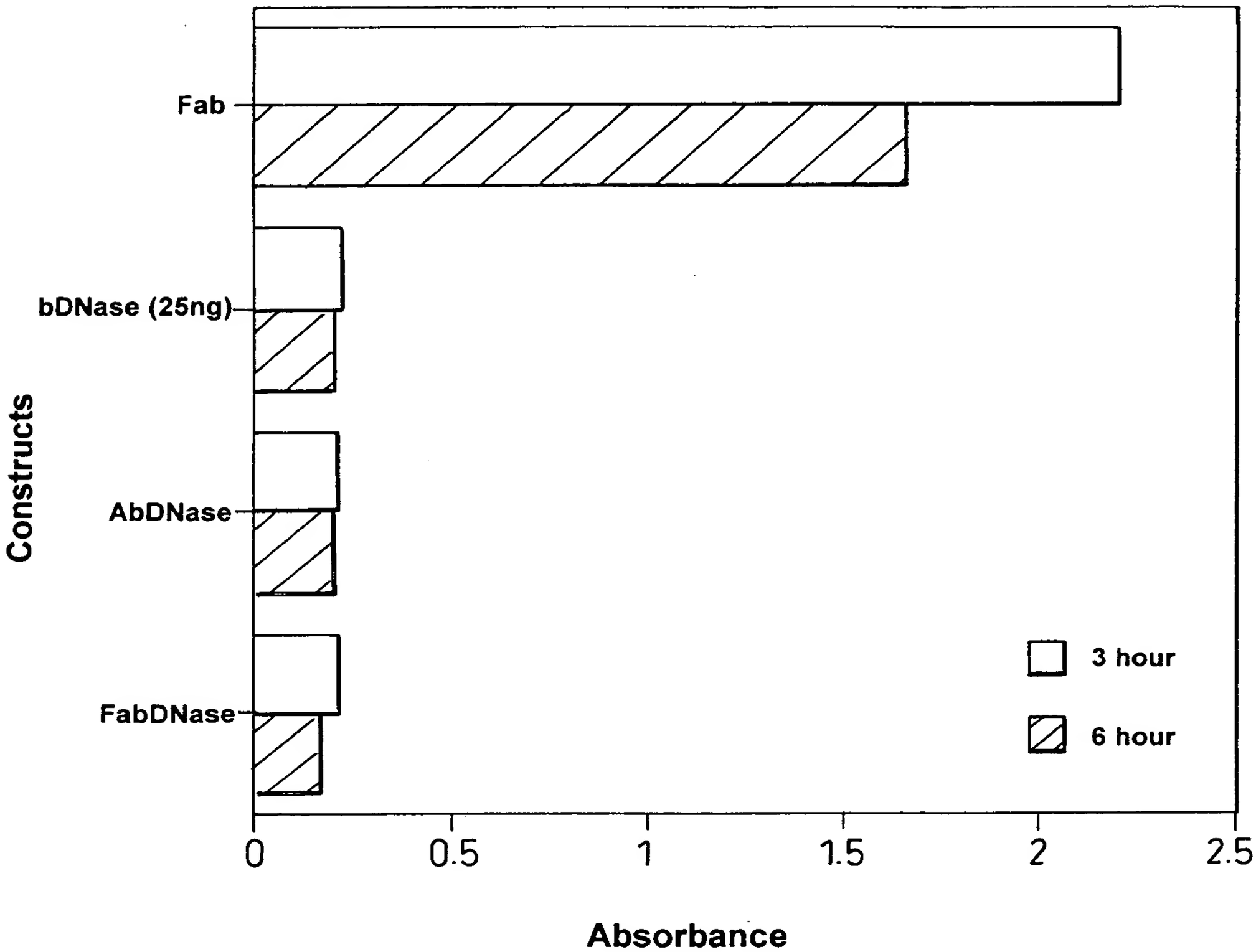

Fab
bDNase (25ng)
AbDNase
FabDNase
Constructs
3 hour
6 hour
0
0.5
1
1.5
2
2.5
Absorbance

Fig. 34(B)

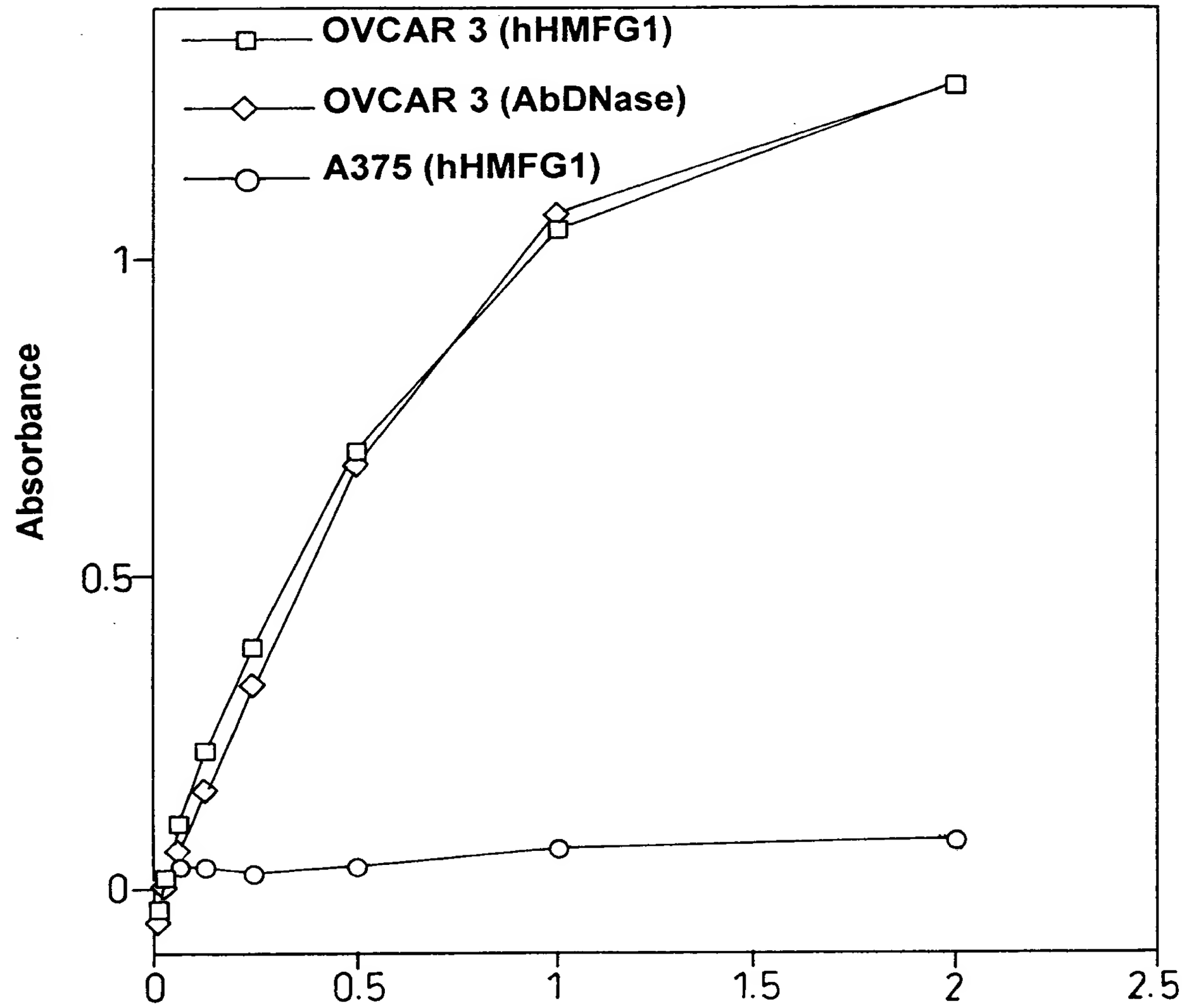

OVCAR 3 (hHMFG1)
OVCAR 3 (AbDNase)
A375 (hHMFG1)
Absorbance
0
0.5
1
0
0.5
1
1.5
2
2.5
Conc. (μg/ml)

Fig. 35(A)

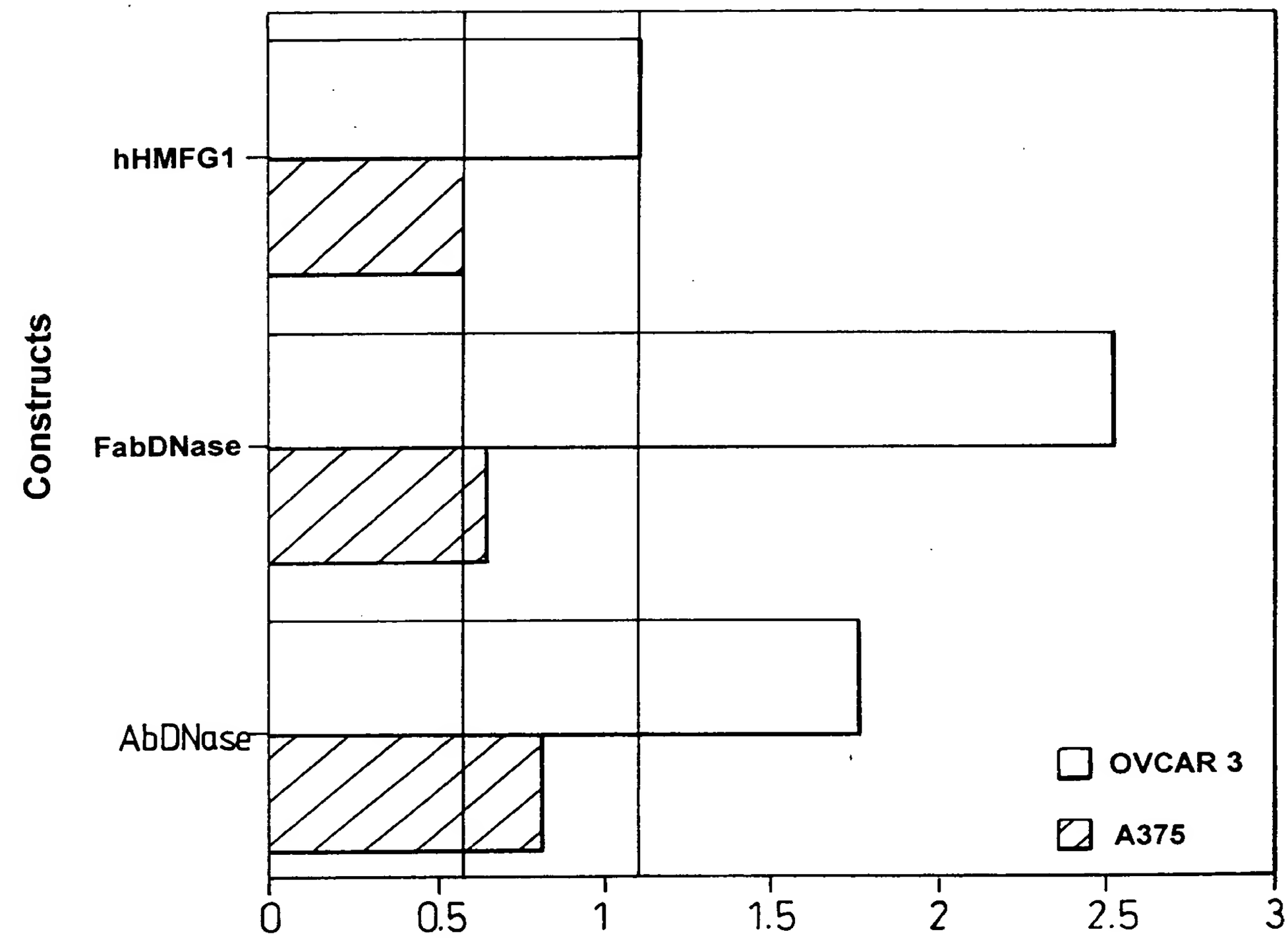

hHMFG1
FabDNase
AbDNase
Constructs
OVCAR 3
A375
0
0.5
1
1.5
2
2.5
3
Absorbance

Fig. 35(B)